

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: January 30, 2004, 22:33:45 ; Search time 4088 Seconds (without attachments)

(without alignments)
11108.044 Million cell updates/sec

Title: US-09-898-456-6
Page: 110

Sequence: 1 atgctgtgtcctgcattcagtcg.....tgggtcaaggcgacgtgcctga 1110

Scoring table: IDENTITY_NUC

Gapor 10.0 , Gapext 1.0

Searched: 288871 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum	DB	seq	length:	0
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Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database

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score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	989.6	89.2	1498	9	AB057725	AB057725 Homo sapi
2	989.6	89.2	1650	6	AX298282	AX298282 Sequence
3	988	89.0	1064	6	AX350382	AX350382 Sequence
4	974	87.7	1597	6	AY009402	AY009402 Homo sapi
5	969.4	87.3	1245	6	AX153809	AX153809 Sequence
6	741.6	66.8	1747	10	MMNWT8BPT	268889 M. musculus
7	708.4	63.8	1245	6	AX153811	AX153811 Sequence
8	569.4	51.3	1734	6	GGU02097	U02097 Gallus gall
9	547	49.3	149172	9	AC004826	AC004826 Homo sapi
c 10	547	49.3	166870	9	AC113382	AC113382 Homo sapi
c 11	542.2	48.8	217608	2	AC144871	AC144871 Pan trogl
12	537.8	48.5	1749	4	AF308871	AF308871 Ambystoma
c 13	535	48.2	144402	2	AC021854	AC021854 Homo sapi
c 14	533.6	48.1	1598	5	XLXNMT8	X521234 X. laevis Xw
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17	436.2	39.3	1994	9	AB076337	AB076337 Homo sapi
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19	434.6	39.2	2119	6	AX597133	AX597133 Sequence
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22	433	39.0	1634	10	AF130349	Y11094 H. sapiens m
23	417	37.6	71141	2	AC025365	AC025365 Homo sapi
24	415.4	37.4	885	9	HSMTN8B	AX91940 H. sapiens m
25	389	35.0	191880	2	AC133619	AC133619 Rattus no
26	389	35.0	254734	2	AC133619	AC133619 Rattus no
27	384.4	34.6	201643	10	AC074335	AC074335 Mus muscu
28	317.8	28.6	1472	3	AF206500	AF206500 Branchios
29	306.4	27.6	1516	3	AF190470	AF190470 Branchios
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31	232.8	21.0	7552	5	AY033749	AY033749 Danio rer
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ALIGNMENTS

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LOCUS	AB057725	1498 bp	mRNA	linear	PRI 23-JUN-2001
DEFINITION	Homo sapiens mRNA for WNT8A, complete cds.				
ACCESSION	AB057725				
VERSION	AB057725.1	GI:14495175			
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1 (sites)				
TITLE	Salich, T. and Katoh, M.				
JOURNAL	Molecular cloning and characterization of human WNT8A				
	Int. J. Oncol. 19 (1), 123-127 (2001)				

MEDLINE 21301559
PUBMED 11408932
REFERENCE 2 (bases 1 to 1498)
AUTHORS Katoh, M.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-2001) Masaru Katoh, National Cancer Center
Research Institute, Genetics and Cell Biology Section, Genetics
Division, Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045, Japan
(E-mail: mkatoh@ncc.go.jp, Tel: 81-3-3542-2511)

FEATURES

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location/Qualifiers

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6. 1061

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BASE COUNT

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ORIGIN

Query Match 89.2%; Score 989.6; DB 9; Length 1498;
Best Local Similarity 99.6%; Pred. No. 1.3e-283;
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126 ACTAGTGTGGCTTTGGGTGCCAGAGTGGCAATCGAAGAGTGCAGATTCCAGTTGGCTTG 185
235 GAAOGCTGGAACTGCCCTGAAAATGCTCTTCAAGCTCCCAACCAAGGCTGAGAGT 294
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295 GCTACCAAGAGACTTCTTCAATCATGATCATGCTCTGCTGAGTCATGATCATC 354
246 GCTACCAAGAGACTTCTTCAATCATGATCATGCTCTGCTGAGTCATGATCATC 305
355 ACCAAGAACTGTAGATGGGTGATCTTGAAAATCTGGCTGTGATGGGTCAAAACATGGA 414
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415 AAAACGGAAGCAATGCTGATCTGGGAGGCTGCAACCAATGTGAAATTTGGGAA 474
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RESULT 2
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LOCUS AX298282 1650 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 1 from Patent WO0183543.
ACCESSION AX298282
VERSION AX298282.1 GI:17128299
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
AUTHORS Duecker, K.
TITLE Human wingless-like gene
JOURNAL Patent: WO 0183543-A1 08-NOV-2001;
MERCK PATENT GmbH (DE)
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source
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BASE COUNT

423 a 384 c 460 g 383 t

ORIGIN

Query Match 89.2%; Score 989.6; DB 6; Length 1650;
Best Local Similarity 99.6%; Pred. No. 1.3e-283;
Matches 992; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 3
AX350382
LOCUS AX350382 1064 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 7 from Patent WO0181578.

ACCESSION AX350382
VERSION AX350382.1 GI:18616035
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS
1 Vernier, C.A., Fernandes, E.R., Gerlach, V., Shinkets, R.A.,
Malynkar, U.M., Boldog, F.L., Zierhusen, B.D., Spytek, K.A.,
Majumder, K., Tchernev, V.T., Padigan, M., Paturajan, M.,
Burgess, C.E., Gangoli, E.A., Smlthson, G., Rastelli, L.,
Macdougall, J.R., Taupier, R.J., Grosse, W.M., and Alsbrook, J.P.
Novel proteins and nucleic acids encoding same
Patent: WO 0181578-A 7 01-NOV-2001;
Curegen Corporation (US)
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Best Local Similarity 99.5%; Pred. No. 3,7e-283;
Matches 991; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Db 1024 GGCAGTCCCAAGTCCCTGCTGAGTAAAGGCGAGTGCCTGA 1059

RESULT 4
AY009402 1597 bp mRNA linear PRI 13-DEC-2000
LOCUS Homo sapiens WNT8d precursor (WNT8d) mRNA, complete cds.
DEFINITION AY009402 GI:11693045
VERSION AY009402.1 GI:11693045
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1597)
Testa, T. T., Mossakowska, D. E., Carter, P. S., Hu, E., Zhu, Y., Keiseli, D. P., Murdoch, P. R., Herrity, N. C., Lewis, C. J., Cross, D. A., Culbert, A. A., Reith, A. D. and Barnes, M. R.
Molecular cloning and characterization of six novel human WNT genes
2 (bases 1 to 1597)
Unpublished
Barnes, M. R.
Direct Submission
Submitted (18-AUG-2000) Genomic Bioinformatics, Biotechnology and Genetics, Neuroscience and Renal Pharmacology, Smithkline Beecham Pharmaceuticals, New Frontiers Science Park (North), Third Avenue, Harlow, Essex CM19 5AW, UK
LOCATION/Qualifiers
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ORIGIN
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Best Local Similarity 99.5%; Pred. No. 5, 9e-279;
Matches 977; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 415 AAAACAGAGAGCCATGGCTGATCTGGAGGCTGACAGCAATGTGAAATTTGGGGAA 474
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RESULT 5
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LOCUS AX153809 1245 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1 from Patent WO0138353.
ACCESSION AX153809
VERSION AX153809.1 GI:14535436
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS Holloway, J. L.
JOURNAL Human wnt gene
Patent: WO 0138353-A 1 31-MAY-2001;
Zymogenetics, Inc. (US)
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Query Match 87.3%; Score 969.4; DB 6; Length 1245;
Best Local Similarity 99.4%; Pred. No. 1,4e-277;
Matches 973; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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LOCUS MMNT8DPT 1747 bp mRNA linear ROD 01-JUL-1996
DEFINITION M.musculus mRNA for wnt-8D protein.
ACCESSION 268889
VERSION 268889.1 GI:1419029
KEYWORDS wnt-8D protein.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
AUTHORS Boullier, P., Oulad-Abdelghani, M., Bromer, S., Dolle, P. and
Chambon, P.
Wnt-8D: a novel mouse Wnt-8 gene induced by retinoic acid in P19
embryonal carcinoma cells
TITLE
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1747)
AUTHORS Boullier, P.
DIRECT SUBMISSION
JOURNAL Submitted (23-JAN-1996) Philippe Boullier, I.G.B.M.C., 1 Rue
Laurent Fries, Illkirch, 67404, France
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Matches 837; Conservative 0; Mismatches 159; Indels 0; Gaps 0;
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LOCUS AX153811
DEFINITION Sequence 3 from Patent WO0138353.
ACCESSION AX153811
VERSION AX153811.1 GI:14535438
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Holloway, J.L.
TITLE Human wnt gene
JOURNAL Patent: WO 0138353-A 3 31-MAY-2001;
ZymoGenetics, Inc. (US)
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Best Local Similarity 56.5%; Pred. No. 1.1e-199;
Matches 564; Conservative 258; Mismatches 176; Indels 0; Gaps 0;
QY 96 CTGCTCACTTTTCTCTTTTGTGAGTCACTGAAACATTTCTGATTAACAGCTCCCA 155
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DB 102 RGCNTATTTTACATTAACACGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 161
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DB 162 YAAATTCATTTGCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 221
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QY 456 CAATGTGGAATTTGGGAGAAAGATCTTCCAACTCTTTTGGAGCAATTTGGAGAAAGGAGAA 515
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Db	462	RGATGCMGNCNTTNATGAAYYTNCAYAAATATMGNCNGNNGNTTNGCNGTNGC	521
Qy	576	CACCATGAAAAAGACATGCAAAATCATGCGATCTCTGGAGCTGCAGCATACAGATG	635
Db	522	NACNATGAABRGNAACNTGYAARTGYCAATGGNATHMNGNMSNTGYMSNATHCARACNTG	581
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Qy	816	ATCACCGATTAAGTACTGTAAGTCAATTCAGGCTGGGATCTATAGGCACAGAGGGTCTGTA	875
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Qy	996	CAAAATTCAGAGGTGCTGTAAGGTCAAGTGAACAGTGAACAGTGAAGTGGATGGTGAACAA	1055
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Qy	1056	TTACTGGCAGACGTCCCGCAGGACAGTGGCCCAATCCCTGG	1093
Db	1002	YTAATGYGCMNGMNSNCGNMGNSGNCARMSYTTNG	1039
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DEFINITION	U02097		
ACCESSION	U02097.1	GI:403577	
VERSION			
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FEATURES			
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Best Local Similarity	75.1%; Prid. No. 3,4e-158;	
Matches 711; Conservative	0; Mismatches 236; Indels 0; Gaps . 0;	
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Dy	482 CCAAAATCTTTGTGTGACAGTTTTGAGAGAGGGAAGATGTCACAGCCCTGATGAATTTTC 541	
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Dy	782 CTAGCCGAGAGGGGGAACCTGATCTTTTAAAGGAATACACAGATTAACGATACCTGCAATT 841	
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Db      939 CTGAGTGGGAGCGGAGAGGAGCTGCGGCGGCTCTGACGGAGTGGGCTCAAAAGTGAAG 998
QY      962 AGAGAAACTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1021
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RESULT 9
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LOCUS      AC004826
DEFINITION  Homo sapiens PAC clone RPI-309D19 from 5, complete sequence.
ACCESSION  AC004826
VERSION     AC004826.3  GI:7767904
KEYWORDS
SOURCE      HTG.
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            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 149172)
AUTHORS    Sulston,J.E. and Waterston,R.
TITLE      Toward a complete human genome sequence
JOURNAL    Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE    99063792
PUBMED     9847074
REFERENCE   2 (bases 1 to 149172)
AUTHORS    Oersky,P., Goela,D., Edwards,J. and Harper,M.
TITLE      The sequence of Homo sapiens PAC clone RPI-309D19
JOURNAL    Unpublished
REFERENCE   3 (bases 1 to 149172)
AUTHORS    Waterston,R.H.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-1998) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4 (bases 1 to 149172)
AUTHORS    Waterston,R.H.
TITLE      Direct Submission
JOURNAL    Submitted (10-MAY-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5 (bases 1 to 149172)
AUTHORS    Waterston,R.H.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   6 (bases 1 to 149172)
AUTHORS    Waterston,R.
TITLE      Direct Submission
JOURNAL    Submitted (07-OCT-2000) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
            On May 10, 2000 this sequence version replaced gi:7630755.

COMMENT
-----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.wustl.edu
-----
Summary Statistics
-----
Center project name: H_DU0309D19

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping

```

clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
This clone was derived from human PAC library RPI-1, prepared by
Pieter de Jong and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu) using the method described by
Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from
one male donor.
The clone may be obtained either from Genome Systems, Inc.
(http://www.genomesystems.com) or Research Genetics, Inc.
(http://www.resgen.com); or from Pieter de Jong.
VECTOR: pCYPAC2
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RPI1-505H15. Actual start of
this clone is at base position 1 of RPI-309D19; actual end is at
base position 149172 of RPI-309D19.
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repeat_region

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EST AW63893 (NID:G7456432) h173c01.x1"

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Best Local Similarity 100.0%; Pred. No. 2,4e-151;
Matches 547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 14964 GGCAGTGAGAGCCACCATGAAAAGACATGCAAAATGTCATGCTCTTGGAGCTGCAG 15023
QY 624 CATACAGACATGCTGGGTGAGCTGAGTAAATCCGGAGATGGAGACTACCTAAAGGC 683
DB 15024 CATACAGACATGCTGGGTGAGCTGAGTAAATCCGGAGATGGAGACTACCTAAAGGC 15083
QY 684 CAAATGACACAGCCGCTGAAAATGAAATGATTAAGCCGACCTGAGACTGGAAACAG 743
DB 15084 CAAATGACACAGCCGCTGAAAATGAAATGATTAAGCCGACCTGAGACTGGAAACAG 15143
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QY 924 TGGGCGCTGTGACATGATGTGGCTGACAGTGAAGAGAGAAAATGAGTCTATAG 983
DB 15324 TGGGCGCTGTGACATGATGTGGCTGACAGTGAAGAGAGAAAATGAGTCTATAG 15383
QY 984 CAGCTGAATCTGAATTCAGTGTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 1043
DB 15384 CAGCTGAATCTGAATTCAGTGTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 15443
QY 1044 GGTGAGCAAGTATTAATGCGCAGCTCCCGAGAGAGTCCAGTCTCTGGTAAAGGACAG 1103
DB 15444 GGTGAGCAAGTATTAATGCGCAGCTCCCGAGAGAGTCCAGTCTCTGGTAAAGGACAG 15503
QY 1104 TGCCTGA 1110
DB 15504 TGCCTGA 15510

RESULT 10
AC113382 166870 bp DNA linear PRI 28-JAN-2003
LOCUS AC113382
DEFINITION Homo sapiens chromosome 5 clone RP11-325L7, complete sequence.
ACCESSION AC113382
VERSION AC113382.2 GI:27923635
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 166870)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 166870)
AUTHORS DOE Joint Genome Institute.
TITLE DOE Joint Genome Institute.
JOURNAL Direct Submission
REFERENCE 3 (bases 1 to 166870)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Submitted (28-JAN-2003) DOE Joint Genome Institute, 2800 Mitchell
JOURNAL Drive, Walnut Creek, CA 94598, USA
COMMENT On Jan 28, 2003 this sequence version replaced gi:19033496.
Draft Sequence Produced by DOE Joint Genome Institute
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QY 275 CCCACAAACAGCTGAGAGTGTCTACAGAGAGCTTCTTATCATGCTATCAGCTCTG 334
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QY 335 CTGAGCTGATGATCATATCAACCAAGACTGTAGCTGATGCTTGGAAACCTGTGGCT 394
Db 324 CCGGAGCATGTATCAGCTCTGACCGAGAACTGACAGCTGGGAGCTTGCACAACTGCGCT 383
QY 395 GTGATGGGTCAACATGAGAAAAACAGAGGACCATGCTGATCTGGGAGGCTGACAGC 454
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QY 515 AGGATGCGAAGCCCTGATGATTTTCAACAAACAGGCGCGGACACTGGCACTGAGAG 574
Db 504 AAGACTCAAGAGCTTTGATGAACTCCACAAACATGAAAGCAGGAGATTGTCTGCAAT 563
QY 575 CCAACATGAAAAGAGCATGCAATGTCATGSCATCTCGGAGCTGAGCATACAGCAT 634
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Db 624 GCTGCTGCACTGCGAGAGTTGAGGATATAGGCAATTTATGAATTAACACAGACC 683
QY 695 AGGCGCTGAATTAATGAAATGATTAAGCGGAGCTGAGAGCTGGAAACAGCGCCGAGGCC 754
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QY 815 AATCACAGATTAATGATCTGCAATTCAGCTGAGCTGAGCTATGAGCAAGAGGCTGTG 874
Db 804 ACTGCGCGGACTACTGCTGAGAAACGCGAGCTCGGGCTCAAGGACAGAGGCGCGG 863
QY 875 AGTGCCTTACAGAACGCCACAAACATTCAGTGGAGCGACGATGCTGTGGCGCTGT 934
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QY 935 GCATGAGTGTGGCTGAGTGGAGAGAGAGAACTGAGTCAATGAGCATGCTGTAAT 994
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RESULT 13
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LOCUS Homo sapiens chromosome 5 clone RP11-505H15, WORKING DRAFT
DEFINITION SEQUENCE, 21 unordered pieces.
ACCESSION AC021854
VERSION AC021854.3 GI:7658486
KEYWORDS HTG; HTG_PHASE1; HTG_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eulacheia; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 144402)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone

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JOURNAL REFERENCE AUTHORS TITLE JOURNAL

Unpublished
2 (bases 1 to 144402)
Waterston,R.H.
Direct Submission
Submitted (20-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Apr 28, 2000 this sequence version replaced gi:7024086.

COMMENT

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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0505H15
----- Summary Statistics -----
Sequencing vector: plasmid, 28%
Chemistry: Dye-terminator Big Dye, 28% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 13476 bases at least Q40
Consensus quality: 137492 bases at least Q20
Insert size: 15600; agarose-fp
Quality coverage: 3.42 in Q20 bases; sum-of-consigs
Quality coverage: 3.82 in Q20 bases; sum-of-consigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1445: contig of 1445 bp in length
1446 1445: gap of unknown length
1446 3851: contig of 2306 bp in length
3852 3951: gap of unknown length
3952 6428: contig of 2477 bp in length
6429 6528: gap of unknown length
6529 7846: contig of 1318 bp in length
7847 7946: gap of unknown length
7947 10364: contig of 2418 bp in length
10365 10464: gap of unknown length
10465 13198: contig of 2734 bp in length
13199 13298: gap of unknown length
13299 15320: contig of 2022 bp in length
15321 15420: gap of unknown length
15421 18740: contig of 3320 bp in length
18741 18840: gap of unknown length
18841 22611: contig of 3771 bp in length
22612 22711: gap of unknown length
22712 26922: contig of 4211 bp in length
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27023 32530: contig of 5508 bp in length
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32631 39868: contig of 7238 bp in length
39869 39968: gap of unknown length
47269 47369: contig of 7301 bp in length
47370 55269: gap of unknown length
55269 55369: contig of 7900 bp in length
55370 62905: gap of unknown length
62906 63006: gap of unknown length
63007 71007: contig of 7902 bp in length
71008 81750: gap of unknown length
81751 81850: contig of 10743 bp in length
81851 96456: contig of 14606 bp in length
96457 96556: gap of unknown length

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FEATURES
 source
 * 96557 112579: contig of 16023 bp in length
 * 112580 112679: gap of unknown length
 * 112680 129486: contig of 16807 bp in length
 * 129487 129586: gap of unknown length
 * 129587 144402: contig of 14816 bp in length.
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 Matches 546; Conservative 0; Mismatches 0;
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 QY 624 CATACAGACATGCTGCTGACGCTGCTGAATTCGGGAGATGGAGACTAAGGC 683
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RESULT 14

LOCUS XLXNNT8 1598 bp mRNA linear VRT 11-MAY-1994
 DEFINITION X.laavis Xwnt-8 mRNA.
 ACCESSION X57234
 VERSION X57234.1 GI:486620
 KEYWORDS Xwnt-8 gene.
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus.

REFERENCE
 AUTHORS Christian, J.L., McMahon, J.A., McMahon, A.P. and Moon, R.T.
 TITLE Xwnt-8, a Xenopus wnt-1/int-1-related gene responsive to mesoderm-inducing growth factors, may play a role in ventral mesodermal patterning during embryogenesis
 JOURNAL Development 111 (4), 1045-1055 (1991)

MEDLINE
 PUBMED 91347916
 1879349

REFERENCE
 AUTHORS Moon, R.T.
 TITLE Direct Sublimation
 JOURNAL OF PHARMACOLOGY, SJ-30, SEATTLE WA 98195, USA
 OF PHARMACOLOGY, SJ-30, SEATTLE WA 98195, USA
 revised by [3] MAT

REMARK
 Moon, R.T.
 Direct Sublimation
 Submitted (10-MAY-1994) R.T. Moon, UNIVERSITY OF WASHINGTON, DEPT.
 OF PHARMACOLOGY, SJ-30, SEATTLE WA 98195, USA
 On May 13, 1994 this sequence version replaced gi:65266.

FEATURES

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gene

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LEMDKRMSPNSANDNGAIDAPASSASSELLFLRSPYCKNLSLIGOGREGR
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HFCARRRDSNMNTRKRNHR"

BASE COUNT      494 a      310 c      383 g      411 t

Query Match      48.1%; Score 533.6; DB 5; Length 1598;
Best Local Similarity 70.7%; Pred. No. 1.6e-147;
Matches 710; Conservative 0; Mismatches 294; Indels 0; Gaps 0;

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153 CAAAGCCTATCTGACCTACACAGACTAGTGGCCCTTG3GTGCCAGAGTGCATGAGA 212
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156 CAAGGCAATCTGACATACACAGAGTGGTCCGCGGTGGCCAGAAATGGAATGAGA 215
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213 GTGCAAGTTCAGTTTCTTGGGAAAGCTGGAATGCCCTGAAATGCTCTTCACTCTC 272
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216 GTTAATATATCAAGTTTCGTGGGAAATGGAATGGCTGAAAGTACCTGCAAGCTTGC 275
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273 CACCCACAAGAGGTGGAAGTGTACACAGAGACTTCTCTACATAGCTATCAGCTC 332
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276 TACCCACAATGAGACTTGGAAAGTGAACCAAGAAACCTCTTGTGATGCCATTAATC 335
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333 TGCTGAGTATGATCATCATCAACAAAGACTGAGAGTGTGACTTGGAAATCTGTGG 392
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336 AGCGGAGTATGATGATACATGAGAAAGACTGAGAGTGGGAGCTTGTGATCTGTGG 395
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393 CTGTGATGGGTCAAAACATGGAAGAAAGAGGCTGATGATCTGGGAGGCTTCCAG 452
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633 ATGTGCTGAGCTGAGTGTGATTTCCGGGAGATGGAGACTACCTAAAGGCGCAGTATGA 692
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
636 TTGCTGGCTTCAGCTGGCGAGTTTCGGGATATTGGCAATGACTTAAGATCAAGCAGCA 695
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
693 CCAAGCCTGTAATAATGATAAGCGGACGCTGAGAGCTGGGAAACAGCGCCGAGGG 752
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
696 CCAAGGCTAAAGCTTGAAGATGACAAAGAGAAATAGAGTCCGGTAAACAGTGTGCAA 755
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
753 CCACTGGGTGCGCGCTGAGGCTTCTTCTTCTGAGCGAGAGGCGGAACTGATCTTTTGA 812
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
756 CAGAGGAGCATCGCTGATGCTTCAGTTCTGTGGCGGAGCTGAACTTATTTTCTCGA 815
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
813 GGAATACCGAGATACGTAACCTGCAATTCAGGCTGGGACATCTATGACACAGAGGGTGC 872
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
816 AGACTCTCCGATTAATGCTTAAATAACATATGTTTGGTCTCCAGGGGAGAGGAGCG 875
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
873 TGAATGCTTACAGAACAGCCAAACACATCCAGGTGGGAGCGAGTGTGTGGCGCCT 932
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db      876 AGATGCTCTGCAAGATGCGAAGAACTTGTCCAGTGGGAGAGAAAGCTGCAAGAGGCT 935
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      933 GTGCACTGAGTGTGGGCTGCGAGCTGGAGAGAGAGAAACTGAGGTATTAAGCAGCTGTA 992
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      936 TTTCACAGACTGCGGGCTCCGAGTGAAGAGAGAAAGACGAGATTAATCATGATGCTGCA 995
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      993 CTGCAATTCCTCACTGAGTGTGTAACCGTCAAGTGTGACCAAGTGAAGCATGTGGTGACCA 1052
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      996 CTCAATTTCACTGGTGTGCGACAGTCAATGCGAGCAATGCAACAGAGTAGTATTA 1055
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      1053 GTATTACTGGGACGCTCCCGAGGAGTGGCCAGTCCCTGGGTA 1096
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1056 GCATTTCTGGCGCAGAGGAGGAGGAGATTCACATGCTGAATA 1099
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
DRU10869      3022 bp      mRNA      linear      VRT 05-DEC-2001
LOCUS      Danio rerio wnt8-like protein 1 and wnt8-like protein 2 (wnt8)
DEFINITION      mRNA, complete cds.
ACCESSION      U10869 AY032748
VERSION      U10869.2 GI:14574562
KEYWORDS
SOURCE
ORGANISM
Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 1215)
Kelly,G.M., Greenstein,P., Erezylmaz,D.F. and Moon,R.T.
Zebrafish wnt8 and wnt8b share a common activity but are involved
in distinct developmental pathways
Development 121 (6), 1787-1799 (1995)
MEDLINE      95324404
7600994
2 (bases 10 to 1215)
Kelly,G.M.
Direct Submission
Submitted (14-JUN-1994) Pharmacology, University of Washington,
Seattle, WA 98195, USA
3 (bases 1 to 3022)
Levken,A.C., Thorpe,C.J., Waxman,J.S. and Moon,R.T.
Zebrafish wnt8 encodes two wnt8 proteins on a bicistronic
transcript and is required for mesoderm and neuroectoderm patterning
Dev. Cell 1 (1), 103-114 (2001)
JOURNAL      21563308
MEDLINE      11703928
REFERENCE
4 (bases 1 to 3022)
Levken,A.C., Thorpe,C.J., Waxman,J.S. and Moon,R.T.
Direct Submission
Submitted (17-APR-2001) HHMI/Pharmacology, University of
Washington, Box 357750, Seattle, WA 98195, USA
REMARK
COMMENT
Sequence update by submitter
On Jun 28, 2001 this sequence version replaced gi:968914.
FEATURES
source
1..3022
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/chromosome="LGXIV"
/clone="wnt8"
/dev_stage="embryo"
1..3022
/gene="wnt8"
3..1102
/gene="wnt8"
/codon_start=1
/product="wnt8-like protein 1"
/protein_id="AAC59697.2"
/db_xref="GI:14574563"
/translation="MNPCCIPLVLSVSIICHHISSTAWSVNFMTPKAYLYTSV
QAAOAGIECKYOFAMERNWCPESALQLSTHNGLSATRETAFAHISAQWYTLT

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XX (MERE) MERCK PATENT GMBH.
PA

PI Duecker K;

DR WPI; 2002-034504/04
DR P-PSDB; AAM47902.

DR P-PSDB; AAM47902.

PT New wingless/int 8D polypeptide, useful for treating asthma,
PT Alzheimer's disease, cancer, ischemia, stroke, depression,
PT schizophrenia, aberrant apoptosis and for identifying modulators of
PT polypeptide activity -
PT

PS Claim 2; Page 35-37; 43pp; English.

CC The invention relates to a polypeptide (I) having a fully defined
CC wingless/int 8D (Wnt-8D) protein sequence of 351 amino acids (AA#47902)
CC or is encoded by a defined polynucleotide sequence (II) of 1650
CC nucleotides (AA#05327) or is a polypeptide having 95% identity to (I) or
CC fragments or variants of above mentioned polypeptides. (I) has
CC antitachymatic, nootropic, neuroprotective, cytostatic, antidepressant,
CC neuroleptic, vasotropic, cerebroprotective and vulnary activity. (I) is
CC useful for identifying compounds that stimulate or inhibit the function
CC or level of the polypeptide. (I) and (II) are useful for treating asthma,
CC Alzheimer's disease, cancer, cardiomyopathies, depression, schizophrenia,
CC general psychotic disorders, ischaemia, stroke, wound healing, kidney
CC diseases, lung disorders, aberrant apoptosis, tissue remodeling, stem
CC cell therapies. (I) and (II) are also useful as vaccines for inducing an
CC immunological response in a mammal and in gene therapy.
CC
CC
SQ Sequence 1650 BP, 423 A, 384 C, 460 G, 383 T, 0 other;

SQ Sequence 1650 BP; 423 A; 384 C; 460 G; 383 T; 0 other;

Query Match	89.28;	Score 989.6;	DB 24;	Length 1650;

Best Local Similarity 99.6%; Pred. No. 6.8e-304;
Matches 992; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY	115	TTTGGTAGGTCAGGTGAACAACTTTCCGTATPAACAGGTCCTCAAGGCTCATCTGACCTCACG	1.74
Db	160	TTGGCTGTCTAGTGAACAATTTCTGTATPAACAGGTCCTCAAGGCTCATCTGACCTCACG	2.19
OY	175	ACTAGTGTGGCCTTGGGATGCCAGATGTGCATGAGAGATGCAAGTTCCAGTTTGGCTTGG	2.34
Db	220	ACTAGTGTGGCCTTGGGATGCCAGATGTGCATGAGAGATGCAAGTTCCAGTTTGGCTTGG	2.79
OY	235	GAAGCTGGAACTGCCCTGAAAAATGCTCTTCACTCTTCCACCCACAACAGGCTGAGAAAT	2.94
Db	280	GAACCTGGAACTGCCCTGAAAAATGCTCTTCACTCTTCCACCCACAACAGGCTGAGAAAT	3.39
OY	285	GCTACCAAGAGACCTTCCTTCATCAATGCTATAGCTCTGCTGAGAGTCATGTATCATCATC	3.54
Db	340	GCTACCAAGAGACCTTCCTTCATCAATGCTATAGCTCTGCTGAGAGTCATGTATCATCATC	3.99
OY	355	ACCAAGAACTGTAGCATGTGGGTGACTTCGAAAACTGTGGCTGTATGGGTCAAAACAATGGA	4.14
Db	400	ACCAAGAACTGTAGCATGTGGGTGACTTCGAAAACTGTGGCTGTATGGGTCAAAACAATGGA	4.59
OY	415	AAAACAGAGGCGCATGTGTCGATCTTGGGAGAGGCTGACGCAACAATGTGAAATTTGGGGAA	4.74
Db	460	AAAACAGAGGCGCATGTGTCGATCTTGGGAGAGGCTGACGCAACAATGTGAAATTTGGGGAA	5.19
OY	475	AGGATCTCCAAACTCTTTTGTGACAGTTTGGAGAGAGGGAAGGATGCCAAGCCCTGATG	5.34
Db	520	AGGATCTCCAAACTCTTTTGTGACAGTTTGGAGAGAGGGAAGGATGCCAAGCCCTGATG	5.79
OY	535	AATCTTCAACAACAGGAGCGGCAACTGGCAGTGAAGGCCAACAATGAAAGAGACATGC	5.94
Db	580	AATCTTCAACAACAGGAGCGGCAACTGGCAGTGAAGGCCAACAATGAAAGAGACATGC	6.39
OY	595	AAATGTCAATGGCATCTCTGGGAGCTCAGACATACAGACATGCTGGCTGCAGCTGGCTGAA	6.54
Db	640	AAATGTCAATGGCATCTCTGGGAGCTCAGACATACAGACATGCTGGCTGCAGCTGGCTGAA	6.99
OY	655	TTCCGGAGATGGAGACTTAACCTAAAGGCCAAGTATGACCAAGGCGCTGAAAAATTTGAATG	7.14

Db	700	TTCCGGAGATGGGAGACTACCTAAAGGCCAAGTATGACACAGGCGCTGAAAATTGAAATG	759
QY	715	GATAAGCGGCAGCTTGAGAGCTGGGAAACAGCCCGAGGGCCACTGGGTTGCCCCCTGAGGCC	774
Db	760	GATAAGCGGCAGCTTGAGAGCTGGGAAACAGCCCGAGGGCCACTGGGTTGCCCCCTGAGGCC	819
QY	775	TTCCCTTCAGCGCAGAGCGCGAACTGATCTTTTAAAGGAATCACACAGATTACTGTACC	834
Db	820	TTCCCTTCAGCGCAGAGCGCGAACTGATCTTTTAAAGGAATCACACAGATTACTGTACC	879
QY	835	TGCATATTCAGCCTGGGCGATCTATGGCACAGAGGGTCGTGAATGCTTACAGAACAGCCAC	894
Db	880	TGCATATTCAGCCTGGGCGATCTATGGCACAGAGGGTCGTGAATGCTTACAGAACAGCCAC	939
QY	895	AACACATTCAGGTTGGAGCGACGTAGCTGTGGGCGCCTGTGCATCTGATGTGGGCTGCAG	954
Db	940	AACACATTCAGGTTGGAGCGACGTAGCTGTGGGCGCCTGTGCATCTGATGTGGGCTGCAG	999
QY	955	GTGGAAGAGAGAAAACCTGAGGTCATTAAAGCAGCTGTAACTGCAAAATTCAGAGTGTCTGT	101
Db	1000	GTGGAAGAGAGAAAACCTGAGGTCATTAAAGCAGCTGTAACTGCAAAATTCAGAGTGTCTGT	105
QY	1015	AACGTCAGTGTGACCAAGTGTAAAGCATTTGGTGAACAAGTATTACTGGCGACGCTCCCA	1077
Db	1060	AACGTCAGTGTGACCAAGTGTAAAGCATTTGGTGAACAAGTATTACTGGCGACGCTCCCA	1111
QY	1075	GGCAGTGCACAGTCCCTGGGTAAAGGGCAGTGCTCTGA	1110
Db	1120	GGCAGTGCACAGTCCCTGGGTAAAGGGCAGTGCTCTGA	1155

RESULT 2
ABA04592

ID	ABA04592	standard; cDNA; 1064 BP
...		

AC ABA04592;

DT 21-FEB-2002 (first entry)

DE MOL4 coding sequence.

KW MOL; G-coupled protei

KW neurodegenerative disorder; immune disorder; cardiac disorder;
 KW cell signal processing; metabolic disorder; diabetes, cancer;
 KW

Cytostatic: Neuroprotective: Antiatherosclerotic: Immunosuppressive: KW
Lung disease; autoimmune disease; developmental disorder; antidiabetic; KW

KW Gene therapy; Vaccine; antiinflammatory; MOL4;
KW Wnt-8-11kb protein; cc

2000

XX

FT	4..1059
CDS	

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E1      /-cag- a
FT      /product= "MOL4"

```

XX
PN W0200181578-A2

XX
BD
01-NOV-2001

XX

XX

PR 28-APR-2000; 2000US-200613P.

PK 28-MAY-2000; 2000US-200780E;
PR 01-MAY-2000; 2000US-201006P.

PR 01-MAY-2000; 2000US-201007E.
PR 01-MAY-2000; 2000US-201236P

PR 01-MAY-2000; 2000US-201238P.
PT 03 MAY 2000 2000TTC 201195D

PR 03-MAY-2000; 2000US-201474P.

PR 25-JUL-2000; 2000US-220591P.
PR 15-SEP-2000; 2000US-232678P.
PR 22-JAN-2001; 2001US-263217P.
PR 30-JAN-2001; 2001US-265160P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Vernet CAM, Fernandes ER, Gerlach V, Shinkets R, Malysankar UM;
PI Boldog FL, Zernhsen BD, Spytek KA, Matsumura K, Tcherney VR;
PI Padigan M, Paturaidan M, Burgess CE, Gangolli EA, Smutcheon G;
PI Rastelli L, Macdougall JR, Taupier RJ, Grose WM, Szekeres ES;
PI Alsobrook JP;
XX
DR WPI; 2002-049278/06.
DR P-PSDB; AAM47662.
XX
XX Novel G-protein coupled receptor-related polypeptides and
PT polynucleotides for diagnosing, preventing and treating cardiomyopathy,
PT atherosclerosis, disorders related to cell signal processing and for
PT identifying modulators -
XX
XX Claim 8; Page 34; 227pp; English.

CC The present invention relates to novel G-coupled protein-receptor related
CC proteins and coding sequences (MOLX where X is a number from 1 to 10,
CC ABNA04589-ABNA04603 and ABNA47659-ABNA47673). MOLX proteins and coding
CC sequences are useful for treating or preventing a MOLX-associated
CC disorder, such as cardiomyopathy, atherosclerosis, disorders related to
CC cell signal processing and metabolic pathway modulation, diabetes and
CC cancer. Additionally, MOLX proteins and coding sequences are useful for
CC preventing and treating a variety of disorders including metabolic
CC disorders, nutritional oedema, chronic and hereditary pancreatitis,
CC obesity, infectious disease, anorexia, neurodegenerative disorders,
CC Alzheimer's disease, Parkinson's disease, stroke, immune disorders,
CC haematopoietic disorders and various dyslipidaemias, metabolic syndrome X
CC and wasting disorders associated with chronic diseases and cancers
CC and cardiac disorders, hypertension, hypercalcaemia, cirrhosis, angiogenesis
CC and wound healing, trauma, glomerulonephritis, hyper and hypothyroidism,
CC multiple sclerosis, lung diseases including asthma, Crohn's disease,
CC scleroderma, autoimmune diseases, developmental disorders and neural tube
CC defects. The present sequence is the coding sequence for MOL4.
CC MOL4 is a Wnt 8-like protein.

5Q Sequence 1064 BP; 269 A; 248 C; 323 G; 224 T; 0 other;

Query Match	89.0%	Score 988	DB 24	Length 1054
Best Local Similarity	99.5%	Pred. NO. 1.7e-303		
Matches 991	Conservative	0	Mismatches 5	Indels 0
				Gaps 0

OY	115	TTTGGTAGGTCAAGTGAACATTTCTCGATGACAGGTCCCAAGGCTCATGACCTACAG	174
Db	64	TCTGCTGTGCTGATGAACAATTTCTCGATGACAGGTCCCAAGGCTCATGACCTACAG	123
OY	175	ACTAGTGTGGCTTTGGGTGCCAGAGTGGCATCGAGAGTGCAGATTTCCAGTTTGGTCTGG	234
Db	124	ACTAGTGTGGCTTTGGGTGCCAGAGTGGCATCGAGAGTGCAGATTTCCAGTTTGGTCTGG	183
OY	235	GAACCTGGAACTGCGCCTGAAATAATGTCTTTCAGCTCTCCACCACCAACAGGCTGAGAAGT	294
Db	184	GAACCTGGAACTGCGCCTGAAATAATGTCTTTCAGCTCTCCACCACCAACAGGCTGAGAAGT	243
OY	295	GCTACCAAGAGACATTCTTCAATCACTGCTATTCAGCTCTGGTGGAGTCATGTACATCATC	354
Db	244	GCTACCAAGAGACATTCTTCAATCACTGCTATTCAGCTCTGGTGGAGTCATGTACATCATC	303
OY	355	ACCAAGAACTGTAGCATGGGTGACTTCGAAAACCTGTGGCTGTGATGGGTCAAAACAATGGA	414
Db	304	ACCAAGAACTGTAGCATGGGTGACTTCGAAAACCTGTGGCTGTGATGGGTCAAAACAATGGA	363
OY	415	AAAAACAGAGGCTATGTGCTGATCTTGGGGAGGCTCAGACGACAAATGTGCAATTTGGGGAA	474
Db	364	AAAAATAGGAGGCTATGTGCTGATCTTGGGGAGGCTCAGACGACAAATGTGCAATTTGGGGAA	423

OY	475	AGGATCTCCAAACCTTTTGTGAGACAGTTTGGAGAAAGGAAAGATGCGCAGAGCCCTGATG	534
Db	424	AGGATCTCCAAACCTTTTGTGACAGTTTGGAGAAAGGAAAGATGCCAGAGCCCTGATG	483
OY	535	AATCTTCAACAACAAGGGCCGGCGAGACTGGCAGTGAAGCCACCATGAAAAAGACATGC	594
Db	484	AATCTTCAACAACAAGGGCCGGCGAGACTGGCAGTGAAGCCACCATGAAAAAGACATGC	543
OY	595	AAATGTCATGCAATCTCTGGGAGCTTGAGCATTAAGACATGCTGGCGTGCAGCTGGTAA	654
Db	544	AAATGTCATGCAATCTCTGGGAGCTTGAGCATTAAGACATGCTGGCGTGCAGCTGGTAA	603
OY	655	TTCCGGGAGATGGGAGACTACTTAAAGGCCAAGATATACCAGGCGCTGAAAAATTGAATG	714
Db	604	TTCCGGGAGATGGGAGACTACTTAAAGGCCAAGATATACCAGGCGCTGAAAAATTGAATG	663
OY	715	GATAAGCGGCGAGCTGAGAGCTGGGACAAGCGCCGAGGGGCCACTGGGTGCCCGCTGAGGC	774
Db	664	GATAAGCGGCGAGCTGAGAGCTGGGACAAGCGCCGAGGGGCCACTGGGTGCCCGCTGAGGC	723
OY	775	TTCTCTTCCCTAGCGGAGAGGCGGAACTGATCTTTTAAAGGAATACACAGATTAATTGTAAC	834
Db	724	TTCTCTTCCCTAGCGGAGAGGCGGAACTGATCTTTTAAAGGAATACACAGATTAATTGTAAC	783
OY	835	TGCAATTCGAGCCCTGGGCATCTATGGGACAGAGGGGTGGTGAAGTGCCTACAGAAACAGCCAC	894
Db	784	TGCAATTCGAGCCCTGGGCATCTATGGGACAGAGGGGTGGTGAAGTGCCTACAGAAACAGCCAC	843
OY	895	AACACATTCGAGGTGGGAGCGACGTAAGCTGTGGGCGCCGTGTGCACCTGAGTGTGGCTGAG	954
Db	844	AACACATTCGAGGTGGGAGCGACGTAAGCTGTGGGCGCCGTGTGCACCTGAGTGTGGCTGAG	903
OY	955	GTGGAAGAGAGAAAACTGAGGTATTAAGCAGCTGTATACTGCAAAATTCAGTGTGCTGT	1014
Db	904	GTGGAAGAGAGAAAACTGAGGTATTAAGCAGCTGTATACTGCAAAATTCAGTGTGCTGT	963
OY	1015	ACGGTCAAGTGTGACCAAGTGAAGGCATGTGGTGAAGCAAGTATTACTGCGGACGCTCCCCA	1074
Db	964	ACGGTCAAGTGTGACCAAGTGAAGGCATGTGGTGAAGCAAGTATTACTGCGGACGCTCCCCA	1023
OY	1075	GGCAGTCCCAAGTCCCTGGGTGAAGGGGAGTGCCTGGA	1110
Db	1024	GGCAGTCCCAAGTCCCTGGGTGAAGGGGAGTGCCTGGA	1059
RESULT 3			
ABQ86140			
ID	ABQ86140	standard; DNA; 1056 BP.	
XX	XX		
AC	ABQ86140;		
XX	XX		
DT	10-SEP-2002	(first entry)	
XX	XX		
DE	Novel human gene. SEQ ID 11.		
XX	XX		
KW	Human; cytosolic; vulnery; antiarteriosclerotic; antiparkinsonian;		
KW	neurotropic; neuroprotective; immunosuppressive; haemostatic;		
KW	antiinflammatory; cardiant; anticulic; virucide; antithyroid;		
KW	cerebroprotective; anorectic; metabolic; vacine; cancer; infection;		
KW	wound healing disorders; atherosclerosis; Parkinson's disease;		
KW	Alzheimer's disease; autoimmune disorder; haematopoietic disorder;		
KW	inflammation; neoplastic disease; nervous system disorder;		
KW	cardiovascular disorders; pancreatitis; respiratory disorder;		
KW	hyperproliferation; systemic autoimmune disease; hyper-immunity;		
KW	developmental abnormality; gastrointestinal ulceration; neuropathy;		
KW	haematological disease; metabolic disease; sperm dysfunction;		
KW	thyroid disorder; hypothyroidism; brain damage; colitis;		
KW	cone photo-transduction deficiency; neurological disease; stroke;		
KW	angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;		
KW	trachea; thymus; lymph node; muscular system; obesity; anorexia;		
KW	growth abnormality; precocious puberty; gene; ss.		
OS	Homo sapiens		

PX	XX		WO200250105-A1.
PN	XX		
PD	XX		27-JUN-2002.
PF	XX		17-DEC-2001; 2001WO-US49232.
PR	XX		19-DEC-2000; 2000US-256710P.
PR	XX		20-DEC-2000; 2000US-257048P.
PR	XX		09-JAN-2001; 2001US-260482P.
PR	XX		30-JAN-2001; 2001US-264922P.
PR	XX		06-FEB-2001; 2001US-266797P.
PR	XX		19-MAR-2001; 2001US-276988P.
PR	XX		04-APR-2001; 2001US-281535P.
PR	XX		08-MAY-2001; 2001US-289622P.
PA	XX		(SMIK) SMITHKLINE BEECHAM CORP.
PA	XX		(SMIK) SMITHKLINE BEECHAM PLC.
PA	XX		(GLAX) GLAXO GROUP LTD.
PI	XX		Agarwal P, Birkeland M, Cogswell JP, Kabnick KF, Lai Y;
PI	XX		Martensen SA, Ritzel SK, Smith RF, Strum JC, Xie Q;
DR	XX		WPI; 2002-508784/54.
DR	XX		P-PsDB; ABP60975.
PT	XX		Secreted proteins and polynucleotides useful as vaccines for preventing
PT	XX		or treating various diseases e.g. cancer, wounds, atherosclerosis,
PT	XX		Parkinson's disease, Alzheimer's disease, infection, autoimmune
PT	XX		disorder -
PS	XX		Claim 2(a); Page 231, 335pp; English.
CC	XX		The invention relates to an isolated polypeptide with signal sequences
CC	XX		which allow it to be secreted extracellularly or membrane associated.
CC	XX		The activity of polypeptides of the invention may be described as,
CC	XX		cystostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic,
CC	XX		cardioprotective, immunosuppressive, haemostatic, antiinflammatory,
CC	XX		neurotrophic, antitumor, vincicid, antithyroid, cerebroprotective, anorectic,
CC	XX		and metabolic. Polypeptides and polynucleotides of the invention are
CC	XX		useful in the treatment, or as a vaccine in the prevention of, cancer,
CC	XX		wound healing disorders, infection, atherosclerosis, Parkinson's disease
CC	XX		and Alzheimer's disease, autoimmune disorder, hematopoietic disorder,
CC	XX		inflammation, neoplastic diseases, nervous system related disorders and
CC	XX		cardiovascular disorders, pancreatitis, respiratory disorder,
CC	XX		hyperproliferation, systemic autoimmune disease, hyper-immunity,
CC	XX		developmental abnormality, gastrointestinal ulceration, neuropathy,
CC	XX		hematological abnormalities, metabolic diseases, sperm dysfunction, thyroid
CC	XX		disorders e.g. hypothyroidism, brain damages, colitis, cone photo-
CC	XX		transduction deficiency, neurological diseases, stroke, angiodenesis,
CC	XX		ovulation disorders, diseases in the spinal cord, thyroid gland, heart,
CC	XX		tiresias, thymus, lymph node and muscular system, obesity, anorexia,
CC	XX		growth abnormalities, and alleviation of precocious puberty. The
CC	XX		sequences given in records ABQ6130-ABQ6184 represent novel human cDNA's
CC	XX		of the invention.
SQ	XX		Sequence 1056 BP; 265 A; 247 C; 322 G; 222 T; 0 other;
Query Match		88.9%; Score 986.4; DB 24; Length 1056;	
Best Local Similarity		99.4%; Pred. No. 5.4e-303;	
Matches 990; Conservative		0; Mismatches 6; Indels 0; Gaps 0	
DY	115	TTTGTAGATCAGTAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	174
DY	116	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	175
DY	117	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	176
DY	118	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	177
DY	119	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	178
DY	120	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	179
DY	121	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	180
DY	122	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	181
DY	123	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	182
DY	124	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	183
DY	125	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	184
DY	126	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	185
DY	127	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	186
DY	128	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	187
DY	129	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	188
DY	130	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	189
DY	131	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	190
DY	132	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	191
DY	133	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	192
DY	134	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	193
DY	135	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	194
DY	136	TCTGCTGTGCTAGTAGAACAATTCTCGATTACAGGTCCTCAAGGCCTATCGACTTACAG	195
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QY	295	GCTCCAGAGAGACTTCCTCCATCATCAATGATATGAGCTCTGCTGGAGCTAGTACATCATC	355
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QY	355	ACCAAGAACTGTACATGAGTGACTTCGAAAACTGTGGCTGTGTATGGGTCAAACAATGA	414
Db	301	ACCAAGAACTGTACATGAGTGACTTCGAAAACTGTGGCTGTGTATGGGTCAAACAATGA	360
QY	415	AAAACAGAGGCCATGGCTGGATCTGGGAGAGCTGACGCCAATGTGGAAATTTGGGGAA	474
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QY	475	AGATCTCCAAACTCTTTGTGACAGTTTGGAGAAAGGGAGAGATGCGACAGCCCTGATG	534
Db	421	AGATCTCCAAACTCTTTGTGACAGTTTGGAGAAAGGGAGAGATGCGACAGCCCTGATG	480
QY	535	AATCTTCACAAACAACAGAGGCCGCGACAGCTGACATGAGCCACATGAAAGACATGC	594
Db	481	AATCTTCACAAACAACAGAGGCCGCGACAGCTGAGTGTAGACCAACATGAAAGACATGC	540
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QY	655	TTCCGGGAGATGGGAGACTACTTAAAGGCCAAGATATACAGAGCGCTGAAAAATGGAATG	714
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QY	775	TTCTCTCTAGCGGAGAGCGGGACATGATCTTTTAAAGGAATACGACATTACTGTACCC	834
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QY	835	TGCAATTCGAGCCCTGGGCATCTATGAGCAGAGAGGTCGTGAGTGCCTTACAGAAACAGCCAC	894
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QY	895	AACACATTCAGAGTGGGAGCGACGATGCTGTGGGCGCTGTGCACTAGTGTGGCTGCAG	954
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QY	955	GTGAAGAGAGGAAAACTGAGGTGATTAAGCAGCTGTAACTGCAAAATTCAGTGGTGCCTGT	1014
Db	901	GTGAAGAGAGGAAAACTGAGGTGATTAAGCAGCTGTAACTGCAAAATTCAGTGGTGCCTGT	960
QY	1015	ACGGTCAAGTGTGACCAAGTGAAGCATGTGGTGAAGCAAGATTAATCTGCGACGCTCCCA	1074
Db	961	ACGGTCAAGTGTGACCAAGTGAAGCATGTGGTGAAGCAAGATTAATCTGCGACGCTCCCA	1020
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AAd06571			
ID	AAd06571 standard; cdna; 1245 BP.		
XX	AAd06571;		
XX	10-AUG-2001 (first entry)		
XX	DE		
XX	Human Wnt3 (Zmnc3) cDNA.		
XX	Human; Zmnc3; gene therapy; cellular signaling; antibody production;		
KW	tissue development; biopharmaceutical; glycoprotein; education tool; ss.		
XX			
XX	Homo sapiens		

FH	Key	Location/Qualifiers
FT	CDS	1..1245
FT		/tag= a
FT		/product= "Zmnt3 protein"
FT		/transl_except= (pos:511..513, aa:Ala)
FT		/note= "CDS does not include stop codon"
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XX		
PN		WO200138353-A2.
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PF		17-NOV-2000; 2000MO-USJ1820.
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PR		22-NOV-1999; 99US-0444788.
XX		
PA		(ZYMO) ZYMOGENETICS INC.
PI		Holloway JL;
XX		
DR		WPI; 2001-367660/38.
XX		
P		P-P9DB; AA002906.
PT		Zmnt3 polypeptides useful for producing antibodies, for biopharmaceuticals, and as educational tools in laboratory practical kits -
XX		
PS		Claim 6; Page 75-77; 82pp; English.
XX		
CC		The present sequence is a cDNA encoding human Wnt3 (Zmnt3) protein which is a cellular signalling molecule. Wnt proteins are a family of secreted glycoproteins, which, in many organisms, have a role in morphological development of tissues in both embryonic and adult contexts. Wnt3 DNA and protein are useful as education tools in laboratory practical kits for genetics and molecular biology, protein chemistry and antibody production, and analysis. Wnt3 protein is useful as an aid to teach preparation of antibodies, identify proteins by Western blotting, protein purification, determining the weight of expressed Zmnt3 polypeptides as a ratio of total protein expressed, identifying peptide cleavage sites, coupling amino acids and carboxyl terminal tags, amino acid sequence analysis and monitoring biological activities of both native and tagged protein in vitro and in vivo. Ab is useful for purifying Zmnt3, and cloning and sequencing the polymucleotides that encodes an antibody, hence in the design of humanised antibodies. Wnt3 DNA is also useful in gene therapy.
SO		Sequence 1245 BP; 318 A; 306 C; 347 G; 274 T; 0 other;
	Query Match	87.3%; Score 969.4; DB 22; Length 1245;
	Beeft Local Similarity	99.4%; Pred. No.1.5e-297;
	Matches 973; Conservative	0; Mismatches 6; Indels 0; Gaps 0
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DB		61 TCTGCTGTGTCAGTAACAATTTCTCGATTACAGGTCCTCAAGCCATCTGAACACAG 120
OY		175 ACTAGTGAGCCCTTGGGTGCCAGAGTGGCATCGAAGAATGCAGATTCCAGTTTGCTTGG 234
DB		121 ACTAGTGAGCCCTTGGGTGCCAGAGTGGCATCGAAGAATGCAGATTCCAGTTTGCTTGG 180
OY		235 GAACGCTGGAATGCCCTGAAAATGCTCTTCACGCTCTCCAACCACACAGGCTGAGAGT 294
DB		181 GAACGCTGGAATGCCCTGAAAATGCTCTTCACGCTCTCCAACCACACAGGCTGAGAGT 240
OY		295 GCTACAGAGACTTCTTCATACATGCTATACAGCTGCTGGAGTCATGTACATCATC 354
DB		241 GCTACAGAGACTTCTTCATACATGCTATACAGCTGCTGGAGTCATGTACATCATC 300
OY		355 ACCAAGAACTGTAGCATGGGTGACTTCGAAAACTGTGGCTGTGATGGGTCAACAATGGA 414
DB		301 ACCAAGAACTGTAGCATGGGTGACTTCGAAAACTGTGGCTGTGATGGGTCAACAATGGA 360
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[illegible]

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XX      03-DEC-2001; 2001US-0005947.
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XX      22-NOV-1999; 99US-166827P.
XX      17-NOV-2000; 2000US-0715993.
XX
XX      (HOLL/) HOLLOWAY J L.
XX
XX      Holloway JL;
XX
XX      WPI; 2003-066796/06.
XX      P-PSDB; ABG72362.
XX
XX      Novel human Zwtnt3 polypeptide useful as aid for identifying proteins by
XX      Western blotting, to teach analytical skills such as mass spectrometry
XX      and circular dichromism, and for identifying peptide cleavage sites
XX
XX      Claim 8; Page 29-31; 37pp; English.
XX
XX      The invention relates to an isolated human Zwtnt3 polypeptide (a wingnut
XX      protein which is a signalling molecule/secreted glycoprotein, found
XX      in the extracellular matrix) that is at least 80% identical to
XX      the protein appearing as ABG72362 sequence (SI) of 415 amino acids,
XX      where the polypeptide specifically binds with an anti-Zwtnt3
XX      antibody, or its fragments. Also included are the Zwtnt3 encoding
XX      nucleic acid (or portion), expression vectors, a recombinant host cell
XX      comprising the vector, the antibody, using Zwtnt3 probes to detect
XX      Zwtnt3 mRNA in a biological sample, an anti-idiotypic antibody that
XX      binds the anti-Zwtnt3 antibody and Zwtnt3 fusion proteins.
XX      Mut overexpression can lead to tumour formation and they are
XX      involved in brain development. Zwtnt 3 is useful as an aid for identifying
XX      proteins by Western blotting, protein purification, determining the
XX      weight of the expressed Zwtnt3 polypeptides as a ratio to total protein
XX      expressed, and for identifying peptide cleavage sites and to teach
XX      analytical skills such as mass spectrometry, circular dichromism, to
XX      determine conformation, especially of the four alpha helices, x-ray
XX      crystallography to determine the three-dimensional structure in atomic
XX      detail, nuclear magnetic resonance spectroscopy to reveal the structure
XX      of proteins in solution. Zwtnt3 is further useful in treating
XX      a subject who lacks an adequate amount of the protein, and also in
XX      veterinary and human therapeutics. The nucleic acids are useful as
XX      polymerase chain reaction (PCR) primers and probes, and to detect the
XX      expression of a Zwtnt3 gene in biological sample, and also to determine
XX      whether a subject's chromosomes contain a mutation in Zwtnt3 gene.
XX      The present sequence is the cDNA encoding human Zwtnt3.
XX
XX      Sequence 1245 BP; 318 A; 306 C; 347 G; 274 T; 0 other;
SQ
Query Match      87.3%; Score 969.4; DB 25; Length 1245;
Best Local Similarity 99.4%; Pred. No. 1.5e-297;
Matches 973; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY      715 GATTAAGCGGAGCTGAGAGCTGGGAAACAGGCGCGGCACTGGGTGCGCGCTGAGGCC 774
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QY      835 TGAATTTCCAGCTGGGCACTTATGGCAGAGAGGCTGTAGTGGCTTACGAAACAGCCAC 894
DB      781 TGAATTTCCAGCTGGGCACTTATGGCAGAGAGGCTGTAGTGGCTTACGAAACAGCCAC 840
QY      895 AACACATCCAGGTGGAGGCGACCTAGCTGTGGCGCTGTGCACTGATGTGGCTGCAG 954
DB      841 AACACATCCAGGTGGAGGCGACCTAGCTGTGGCGCTGTGCACTGATGTGGCTGCAG 900
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DB      901 GTGGAAGAGAGAAAACCTGAGTCAATPAAGCAGCTGTAACTGCAATTTCCAGTGTCTGT 960
QY      1015 ACGGTAAAGTGATCCAGTGTGAGCATGTGTGAGCAAGTATTACTGGCAGCCTCCCA 1074
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DB      1021 GGCAGTGGCCAGTCCCTGG 1039

RESULT 6
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ID      AAD06572 standard; cDNA; 1245 BP.
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XX      AAD06572;
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XX      10-AUG-2001 (first entry)
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XX      Human Wnt3 (Zwtnt3) cDNA degenerate sequence.
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XX      Human; Zwtnt3; gene therapy; cellular signalling; antibody production;
XX      tissue development; biopharmaceutical; glycoprotein; education tool; ss.
XX      Homo sapiens.
XX      W0200138353-A2.
XX      31-MAY-2001.
XX

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OY	288	GAGAAGTCTACCAAGAGACTTCTTCACTATATGCTATCACTCTGCTGGAGTCATGTA	347
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Db	494	CGCGCTCACCGCTCTTGCGCCGAGAGGCACCTTCACCAATTTGGCTGTGATCTCGCATCA	553
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1 RESULT 2
2 US-09-459-774-1
3 Sequence 1, Application US/09459774
4 Patent No. 6287030
5 GENERAL INFORMATION:
6 APPLICANT: Michael Robert Barnes
7 APPLICANT: Tania Tamson Testa
8 TITLE OF INVENTION: NOVEL COMPOUNDS
9 FILE REFERENCE: GP-30193
10 CURRENT APPLICATION NUMBER: US/09/459,774/
11 CURRENT FILING DATE: 1999-12-13
12 EARLIER APPLICATION NUMBER: UK 9828419.3
13 EARLIER FILING DATE: 1998-12-23
14 NUMBER OF SEQ ID NOS: 2
15 SOFTWARE: Fastsq for Windows Version 3.0.
16 SEQ ID NO 1
17 LENGTH: 1050
18 TYPE: DNA
19 ORGANISM: HOMO SAPIENS

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US-09-459-774-1

Query Match	13.5%;	Score 149.4;	DB 3;	Length 1050;
Best Local Similarity	52.0%;	Pred. No. 2.7e-37;		
Matches 386;	Conservative 0;	Mismatches 351;	Indels 6;	Gaps 2;

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OY	310	TCTTTATACATGCTATCAAGCTCTGCTGTGAGATCATGTATCATCATCAAGAACTGTAGC	369
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OY	907	TGGGAGCGACGTAGCGTGGGCG	929
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Sequence 1, Application US/09903817
Patent No. 6515108
GENERAL INFORMATION:
APPLICANT: BARNES, Michael Robert
APPLICANT: TESTA, Tania Tamson
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30193-D1
CURRENT APPLICATION NUMBER: US/09/903,817
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: UK 9826419.3
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 09/459,774

GenCore version 5.1.6
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Listing first 45 summaries

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28: gb_ges1:*
29: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	473.6	42.7	825	28	AQ746299 HS_2277_A
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4	389.6	35.1	685	9	AL651356 AL651356

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14	266.6	24.0	904	14	CD052815
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17	259.2	23.4	503	9	AM460434
18	258.4	23.3	531	12	BG816071
19	258	23.2	623	12	BI888991
20	255	23.0	661	10	BB655336
21	246.4	22.2	697	9	AL594545
22	242	21.8	497	9	AL794001
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24	236	21.3	766	9	AM019457
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28	191	17.2	409	10	BE576612
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31	181.4	16.3	530	9	AM059338
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33	179.8	16.2	483	10	BF732616
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35	162	14.6	898	13	BU543397
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ALIGNMENTS

RESULT 1
LOCUS BC044143 3151 bp mRNA
DEFINITION Danio rerio, clone IMAGE:2600933, mRNA.
ACCESSION BC044143
VERSION BC044143.1 GI:28422285
KEYWORDS
SOURCE
ORGANISM Danio rerio (zebrafish)
HTC
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Osteichthyes;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 3151)
REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbbs-remail.nih.gov
Tissue Procurement: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
CDNA Library Preparation: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
CDNA Library Arrayed by: The I.W.A.G.E. Consortium (ILNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>

contact: amadan@systemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILM; at: <http://image.llnl.gov>
 Series: IRAX Plate: 101 Row: c Column: 3

This clone has the following problem: retained intron.
 Location/Qualifiers

FEATURES

source

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 including unfertilized eggs)"
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 /lab_host="DH10B"
 /note="Vector: PME18S-FL3"

BASE COUNT 913 a 637 c 779 g 822 t
 ORIGIN

Query Match 43.0%; Score 477.2; DB 11; Length 3151;
 Best Local Similarity 68.2%; Pred. No. 1.7e-129;
 Matches 662; Conservative 0; Mismatches 308; Indels 0; Gaps 0;

96 CTGCTCAGCTTTCTCTTTTGTAGTCACTGAAACATTTCTTGATACAGGCTCCAA 155
 136 CTGTACACACTGTGTGTCAACGACATGTGTGTATTAATCTTCGATGACAGCAAA 195
 156 GGCCTATCGACCTACACAGCTAGTGTGCTTGGGTCCAGAGGGCATCGAGAGT 215
 196 GCTTATCTCGCATACACAGAGTGTACAGCTGGGCTCGAGTGTATGAAAGATG 255
 216 CAAGTTCAGTTTGTCTTGGGAAGCTGGAACCTCCCTGAAAATGCTCTTCACTCCAC 275
 256 CAAGATCAGTTCGATGGGACAGGTGGAACTGCCGGAAGCGACATGCAATTCGAC 315
 276 CCACACAGGCTGAGAAAGTGTACCAAGAGACCTTCTTCAATACATGCTATGCTG 335
 316 GATTAAGGCTCGCGAGAGCCACCAAGAGACGCTTGTGCAATGTATTAAGTCTGC 375
 336 TGGAGTCATGTACATCATCAACCAAGACGTAGCATGGGTGATCTGGAACCTGGGCTG 395
 376 TGGAGTTATGTACATTTGACCAAAATCTGCAGCATGGGGACTTGCAGAACTGTGGCTG 435
 396 TGAATGGTCAAACAATGGAAGAAAGAGAGCCATGGCTGATCTGGGAGGCTGCAGCA 455
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 516 GGATGCCAGAGCCGATGAATCTTCAACAAAGAGGCGCGGACAGTGGGAGTGAAGC 575
 556 GCACTCTGCGCGCGGCTCAACCTGATACAAAGAGTGTGATCTGCTTTAAAGC 615
 576 CACCATGAAAAGAGATGCAAAATGTATGATGCTCTGAGAGCTCAGCATACAGACATG 635
 616 AACGCTCAAAAGAGACTGTAACTGTATGTGTTGTCTGGAACCTGTAGATTCAGACATG 675
 636 CTGCTGACAGCTGGCTGAATTCGCGAGATGGGAGACTACTAAAGGCAAGTATGACCA 695
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 756 CTGGTGGCCGCTGAGGCTTCTCTTCTAGCGCAGAGGCGGAATGATCTTTAGAGGA 815

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RESULT 2
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 LOCUS HS 2277 A2 D06 MR CIT Approved Human Genomic Sperm Library D Homo
 DEFINITION sapiens genomic clone Plate=2277 Col=12 Row=G, genomic survey

ACCESSION A0746299
 VERSION A0746299
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 825)
 AUTHORS Mahairas G.G., Wallace J.C., Smith K., Swartzell S., Holzmann T.,
 Keller A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and
 Hood L.

TITLE Sequence-tagged connectore: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 PUBMED 10449764

COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: <http://www.hfsc.washington.edu>
 Plate: 2277 row: G column: 12
 Seq primer: M13 Reverse
 Class: BAC ends

High quality sequence stop: 825.

FEATURES

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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone_image="Plate=2277 Col=12 Row=G"
 /sex="male"
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 /note="Organ: sperm; Vector: pBelOBAC11; BAC clones in
 E-Coli DH10B"

BASE COUNT 210 a 208 c 207 g 180 t 20 others
 ORIGIN
 Query Match 42.7%; Score 473.6; DB 28; Length 825;
 Best Local Similarity 95.5%; Pred. No. 1.1e-128;


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Qy 415 AAAACAGAGAGCCATGGCTGATCTGGGAGGCTGCAGCGACAAATGTGAAATTTGGGAA 474
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RESULT 2

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US-09-842-758-7
; Sequence 7, Application US/09842758
; Publication No. US20030083244A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Fernandes, Silma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shimkels, Richard A
; APPLICANT: Malysankar, Ufiel M
; APPLICANT: Boldog, Ferenc L
; APPLICANT: zerhusen, Bryan D
; APPLICANT: Szytek, Kimberly A
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patnirajan, Meera
```

```
APPLICANT: Burgess, Catherine E
APPLICANT: Gangolli, Esha A
APPLICANT: Smithson, Glenda
APPLICANT: Rastelli, Luca
APPLICANT: Macdougall, John R
APPLICANT: Taupier, Raymond J
APPLICANT: Grose, William M
APPLICANT: Edward, Szekeres S
APPLICANT: Alsobrook II, John P
TITLE OF INVENTION: No. US20030083244A1e1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-783
CURRENT APPLICATION NUMBER: US/09/842,758
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/200,158
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 60/200,613
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,780
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/201,006
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,007
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,236
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,238
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,186
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/201,474
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/201,508
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/220,591
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/232,678
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/263,217
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/265,160
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 1064
TYPE: DNA
ORGANISM: Homo sapiens
US-09-842-758-7
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Best Local Similarity 99.5%; Pred. No. 0;
Matches 991; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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RESULT 3
US-10-285-976-24
Sequence 24, Application US/10285976
Publication No. US20030165500A1
GENERAL INFORMATION:
APPLICANT: Rhee, Chae-Seo
APPLICANT: Malini, Sen
APPLICANT: Wu, Christina
APPLICANT: Leon, Lorenzo M.
APPLICANT: Cort, MariPat
APPLICANT: Carson, Dennis A.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
FILE REFERENCE: 023070-130320US
CURRENT APPLICATION NUMBER: US/10/285,976
PRIOR FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US 60/287,995
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: WO PCT/US02/13802
NUMBER OF SEQ ID NOS: 232
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24

LENGTH: 1597
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human Wnt-8a
US-10-285-976-24

Query Match 87.7%; Score 974; DB 13; Length 1597;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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				Gaps 0

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Db	481	AATCTTCAACAACA	CAGGGCCGGAGACTGCGACGTGAGAGGCCACCATGAAAAAGGACATGC	540
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QY	715	GATTAAGGGGACGCTGAGAGCTGGGGAAACAAGGCGGAGGGCCACTGGGTCGCCGCTGAGAGGC	774
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QY	955	GTCGAGAGGAGGAAACTGAGGTCATTAAGCAGCTGTAACTGCAAATTCAGATGGTGTCTGT	1014
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Db	1021	GGCAGTGCACGATCCCTGG	1039

RESULT 5
US-10-005-947-3
; Sequence 3, Application US/10005947
; Publication No. US20020123103A1

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: GENERAL INFORMATION:
: APPLICANT: Holloway, James L.
: TITLE OF INVENTION: Human Wnt Gene
: FILE REFERENCE: 99-87
: CURRENT APPLICATION NUMBER: US/10/005,947
: CURRENT FILING DATE: 2001-12-03
: PRIOR APPLICATION NUMBER: US/09/715,993
: PRIOR FILING DATE: 2000-11-17
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 1245
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: This degenerate sequence encodes the amino acid
: NAME/KEY: variation
: LOCATION: (1)...(1245)
: OTHER INFORMATION: N is any nucleotide.
: US-10-005-947-3

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Query Match	63.8%	Score 708.4	DB 14	Length 1245
Best Local Similarly	56.5%	Pred. NO. 2.7e-234		
Matches 564	Conservative 258	Mismatches 176	Indels 0	Gaps 0

Oy		96	TGCTCACTTTTCTCTTTTGTAAGTCAGTGAACAATTCGTGAATAACGGGCCAA	155
Db		42	YTGCGNCNTTVSNGCNSMNGNTGMSNGTAAAYATTYYTNATHACNGCNCAA	101
Oy		156	GGCCTATCTGACTACACGACTAGTGTGGCCCTTGSGTGCCACAGATGGCATCGAGA GTG	215
Db		102	RGCTATAYTNACNTHAACHCMNSMNGTNGCYTNGGNCNCARMSNGSNATHGAR GARTG	161
Oy		216	CAGTTCACGTTTGCTTTGGGAACGCTGGAACCTGTGAAAATGCTTTCAGCTCTCAC	275
Db		162	YAATTTYCARITTYGCTNGGGARMGNTGGAAVTGYCCNGARAAYGCVNYTNCARYTWSNA C	221
Oy		276	CCAACAACGGGTGAGAAAGTGCTACCACAGAGACTTCTTCAITACATGTAACAGCTCTGC	335

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Db 222 NCATTAATGNTTNNGNMNGCNACNMGAGACATGNTTATGCAATGATGNTGNGC 281
Qy 336 TGAGATCATGATCATCATCATCAAGAACTGTAGCAGGAGTGTGCTGCTGCTG 395
Db 282 NCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 341
Qy 396 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 455
Db 342 YGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 401
Qy 456 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 515
Db 402 YAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 461
Qy 516 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 575
Db 462 RGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 521
Qy 576 CACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 635
Db 522 NAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 581
Qy 636 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 695
Db 582 YTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 641
Qy 696 GGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 755
Db 642 RGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 701
Qy 756 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 815
Db 702 YTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 761
Qy 816 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 875
Db 762 RMSATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 821
Qy 876 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 935
Db 822 RTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 881
Qy 936 CACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 995
Db 882 YACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 941
Qy 996 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1055
Db 942 YAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1001
Qy 1056 TTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1093
Db 1002 YTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1039
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RESULT 6
US-10-029-386-8756
; Sequence 8756, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 8756
; LENGTH: 600
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004826.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.61
; OTHER INFORMATION: SWISSPROT HIT: Q9H1U5, EVALUE 1.00e-107
; OTHER INFORMATION: EST HUMAN HIT: A1741277.1, EVALUE 1.40e-02
; OTHER INFORMATION: NT HIT: g114781158, EVALUE 0.00e+00
US-10-029-386-8756
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Query Match 49.3%; Score 547; DB 13; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.7e-178;
Matches 547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 564 GGCAGTGAAGCCACCATGAAAGAGCATGCAATGTCATGATGCTGAGAGCTGAG 623
Db 29 GGCAGTGAAGCCACCATGAAAGAGCATGCAATGTCATGATGCTGAGAGCTGAG 88
Qy 624 CATACAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 683
Db 89 CATACAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 148
Qy 684 CAAGTATGACAGGCGCTGAAATTTGAATGATTAAGCGGACCTGAGAGCTGGAA 743
Db 149 CAAGTATGACAGGCGCTGAAATTTGAATGATTAAGCGGACCTGAGAGCTGGAA 208
Qy 744 CGCGAGGCGCATGAGGTCGCGCTGAGGCTTCTTCTTCTTCTTCTTCTTCTTCT 803
Db 209 CGCGAGGCGCATGAGGTCGCGCTGAGGCTTCTTCTTCTTCTTCTTCTTCTTCT 268
Qy 804 CTTTATGAGGATTCACAGATTAATGATGATGATGATGATGATGATGATGATGATG 863
Db 269 CTTTATGAGGATTCACAGATTAATGATGATGATGATGATGATGATGATGATGATG 328
Qy 864 AGAGGTCGTGATGCTTACAGAAACAGCAACACATCCAGTGGAGCGAGCTAGCTG 923
Db 329 AGAGGTCGTGATGCTTACAGAAACAGCAACACATCCAGTGGAGCGAGCTAGCTG 388
Qy 924 TGGGCGGCTGTGATGAGTGTGGGTCGAGGTGGAAGAGAGAGAGAGAGAGAGAG 983
Db 389 TGGGCGGCTGTGATGAGTGTGGGTCGAGGTGGAAGAGAGAGAGAGAGAGAGAG 448
Qy 984 CACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1043
Db 449 CACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 508
Qy 1044 GGTGAGCAAGTATTAATGAGGACGCTCCCGAGCAGTGGCAGTGGGTAAGGGCAG 1103
Db 509 GGTGAGCAAGTATTAATGAGGACGCTCCCGAGCAGTGGCAGTGGGTAAGGGCAG 568
Qy 1104 TGCCTGA 1110
Db 569 TGCCTGA 575
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RESULT 7
US-10-029-386-22482
; Sequence 22482, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 22482
; LENGTH: 546
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GenCore version 5.1.6
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OM nucleic - nucleic search, using BW model

Run on: January 30, 2004, 23:55:41 ; Search time 445 Seconds

(without alignments)
7050.754 Million cell updates/sec

Title: US-09-898-456-6
Sequence: 1 atgcctgcctcattcagtcg.....tgggtaaggcagtcctga 1110

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4893588 seqs, 1413326768 residues

Total number of hits satisfying chosen parameters: 9787176

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	989.6	89.2	1899	1	PCT-US03-37355-57 Sequence 57, App1
2	986.4	88.9	1056	7	US-10-451-168-11 Sequence 11, App1
3	170	15.3	1506	1	PCT-US03-37355-53 Sequence 53, App1
4	164.4	14.8	1047	1	PCT-US03-04188-1 Sequence 1, App1
5	164.4	14.8	1047	7	US-10-364-888-1 Sequence 1, App1
6	164.4	14.8	2160	1	PCT-US03-04188-7 Sequence 7, App1
7	164.4	14.8	2160	7	US-10-364-888-7 Sequence 7, App1
8	163.8	14.7	1070	1	PCT-US03-04188-5 Sequence 5, App1
9	163.8	14.7	1070	7	US-10-364-888-5 Sequence 5, App1
10	162.6	14.6	1002	1	PCT-US03-25100-147 Sequence 147, App
11	162.6	14.6	1014	1	PCT-US03-25100-141 Sequence 141, App
12	162.6	14.6	1014	1	PCT-US03-25100-159 Sequence 159, App
13	162.6	14.6	1056	1	PCT-US03-25100-151 Sequence 151, App
14	162.6	14.6	1059	1	PCT-US02-36071A-60 Sequence 60, App1
15	162.6	14.6	1060	1	PCT-US03-25100-145 Sequence 145, App
16	162.6	14.6	1060	1	PCT-US03-25100-173 Sequence 173, App
17	162.6	14.6	1060	1	PCT-US03-25100-175 Sequence 175, App
18	162.6	14.6	1071	1	PCT-US03-25100-155 Sequence 155, App
19	162.6	14.6	1076	1	PCT-US03-25100-169 Sequence 169, App
20	162.6	14.6	1081	1	PCT-US03-25100-139 Sequence 139, App
21	162.6	14.6	1081	1	PCT-US03-25100-161 Sequence 161, App
22	162.6	14.6	1082	1	PCT-US03-25100-167 Sequence 167, App
23	162.6	14.6	1099	1	PCT-US03-25100-153 Sequence 153, App
24	162.6	14.6	1116	1	PCT-US03-25100-143 Sequence 143, App
25	162.6	14.6	1116	1	PCT-US03-25100-177 Sequence 177, App

26	162.6	14.6	1116	1	PCT-US03-25100-179 Sequence 179, App
27	162.6	14.6	1116	1	PCT-US03-25100-187 Sequence 187, App
28	162.6	14.6	1116	1	PCT-US03-25100-189 Sequence 189, App
29	162.6	14.6	1116	1	PCT-US03-25100-191 Sequence 191, App
30	162.6	14.6	1555	1	PCT-US02-36071A-59 Sequence 59, App1
31	162.6	14.6	2932	1	PCT-US03-25100-157 Sequence 157, App
32	161	14.5	1116	1	PCT-US03-25100-181 Sequence 181, App
33	161	14.5	1116	1	PCT-US03-25100-183 Sequence 183, App
34	161	14.5	1116	1	PCT-US03-25100-185 Sequence 185, App
35	159.4	14.4	1194	1	PCT-US03-25100-165 Sequence 165, App
36	159.4	14.4	1194	1	PCT-US03-25100-171 Sequence 171, App
37	153.4	13.8	2814	1	PCT-US02-36071A-56 Sequence 56, App1
38	152.6	13.7	966	1	PCT-US03-17512-41 Sequence 41, App1
39	152.6	13.7	966	6	US-10-454-246-41 Sequence 41, App1
40	152.4	13.7	849	1	PCT-US03-25100-149 Sequence 149, App
41	151.4	13.6	1059	1	PCT-US02-36071A-57 Sequence 57, App1
42	151	13.6	966	1	PCT-US03-17512-35 Sequence 35, App1
43	151	13.6	966	1	PCT-US03-17512-39 Sequence 39, App1
44	151	13.6	966	6	US-10-454-246-35 Sequence 35, App1
45	151	13.6	966	6	US-10-454-246-39 Sequence 39, App1

ALIGNMENTS

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RESULT 1
PCT-US03-37355-57
; Sequence 57, Application PC/TUS0337355
; GENERAL INFORMATION:
; APPLICANT: Keating et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DIFFERENTIATION AND TISSUE
; FILE REFERENCE: HYDR-PW1-004
; CURRENT APPLICATION NUMBER: PCT/US03/37355
; CURRENT FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-37355-57

Query Match      89.2%; Score 989.6; DB 1; Length 1899;
Best Local Similarity 99.6%; Pred. No. 2.3e-302;
Matches 992; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      115 TTTGTAGTGCAGAACAAATTTCTGATTAACAGTCCCAAGGCTTATGACCTACAG 174
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DB      161 TCTGCTGTGTCAGAACAAATTTCTGATTAACAGTCCCAAGGCTTATGACCTACAG 220

QY      175 ACTAGTGTGGCTTGGTGGCCCAAGTGGCATTCAGAGTGCAGAGTTCAGTTGCTTGG 234
      |||||
DB      221 ACTAGTGTGGCTTGGTGGCCCAAGTGGCATTCAGAGTGCAGAGTTCAGTTGCTTGG 280

QY      235 GAAGCTGGAACCTGCGTGAATAATGCTTCAAGCTTCCACCACAAGAGCTGAGAGT 294
      |||||
DB      281 GAAGCTGGAACCTGCGTGAATAATGCTTCAAGCTTCCACCACAAGAGCTGAGAGT 340

QY      295 GCTACCAAGAGACTTCTTATACATGCTATACAGCTTGTGAGTATGATATCATATC 354
      |||||
DB      341 GCTACCAAGAGACTTCTTATACATGCTATACAGCTTGTGAGTATGATATCATATC 400

QY      355 ACCAAGAACTGTACATGAGTGGTGAATCTGTGCTGTATGGTCAACAATGGA 414
      |||||
DB      401 ACCAAGAACTGTACATGAGTGGTGAATCTGTGCTGTATGGTCAACAATGGA 460

QY      415 AAAACAGAGGCACTGTGATCTGGAGGAGGCTGACGCAATGTGAAATTTGGGGA 474
      |||||
DB      461 AAAACAGAGGCACTGTGATCTGGAGGAGGCTGACGCAATGTGAAATTTGGGGA 520

QY      475 AGATCTCCAAACTTTTGTGACAGTTTGGAGAAGGGAAGATGCGCAGAGCCCTGATG 534
      |||||
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Db 521 AGAATCTCCAACTCTTTGTGGACAGTTTGGAGAGGGAAGATGCCAGCCCTGTATG 580
Qy 535 AATCTTCAACAAAGAGGCGGCGAGACTGGAGTGAAGCCACCATGAAAAAGCATGC 594
Db 581 AATCTTCAACAAAGAGGCGGCGAGACTGGAGTGAAGCCACCATGAAAAAGCATGC 640
Qy 595 AATGTGATGAGCTCTGTGGAGCTGCAGCATACAGATGTGGCTCAGCTGAGTAA 654
Db 641 AATGTGATGAGCTCTGTGGAGCTGCAGCATACAGATGTGGCTCAGCTGAGTAA 700
Qy 655 TTCCGGAGATGGAGACTACCTTAAAGGCCAAGTATGACAGGCGCTGAAAAATTGAATG 714
Db 701 TTCCGGAGATGGAGACTACCTTAAAGGCCAAGTATGACAGGCGCTGAAAAATTGAATG 760
Qy 715 GATTAAGCGGCGAGCTGAGAGCTGGGAAACAGCGCGGAGGCGCACTGGGTGCCGCTTAAAGGCC 774
Db 761 GATTAAGCGGCGAGCTGAGAGCTGGGAAACAGCGCGGAGGCGCACTGGGTGCCGCTTAAAGGCC 820
Qy 775 TTCCCTCTAGCGAGAGGCGGAGCTGATCTTTTAAAGAAATCAACAGATTACTGTACC 834
Db 821 TTCCCTCTAGCGAGAGGCGGAGCTGATCTTTTAAAGAAATCAACAGATTACTGTACC 880
Qy 835 TGCATTTCCAGCTTGGGAGCTGATGAGCAAGAGGCTGAGTGGCTTACAGAAACAGCCAC 894
Db 881 TGCATTTCCAGCTTGGGAGCTGATGAGCAAGAGGCTGAGTGGCTTACAGAAACAGCCAC 940
Qy 895 AACACATCCAGTGGGAGCGAGCTGAGTGGGCGGCTGTGATGAGTGGTGGGCTGAG 954
Db 941 AACACATCCAGTGGGAGCGAGCTGAGTGGGCGGCTGTGATGAGTGGTGGGCTGAG 1000
Qy 955 GTGGAAGAGAGGAAATGAGGTGATTAAGCAGCTGTAATTCAGTGGTGGTGT 1014
Db 1001 GTGGAAGAGAGGAAATGAGGTGATTAAGCAGCTGTAATTCAGTGGTGGTGT 1060
Qy 1015 ACGGTCAAGTGTGACAGTGTAGGAGTGTGTAGCAAGTATTACTGGCGACGCTCCCA 1074
Db 1061 ACGGTCAAGTGTGACAGTGTAGGAGTGTGTAGCAAGTATTACTGGCGACGCTCCCA 1120
Qy 1075 GGCAATGCCAGTCCCTGTGGTAAAGGCGAGTGCCTGA 1110
Db 1121 GGCAATGCCAGTCCCTGTGGTAAAGGCGAGTGCCTGA 1156

RESULT 2
US-10-451-168-11
; Sequence 11, Application US/10451168
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50039
; CURRENT APPLICATION NUMBER: US/10/451,168
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US01/49232
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,710
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/257,048
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/260,482
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/264,922
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/266,797
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/276,988
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/281,535
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/289,622
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 110

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-451-168-11
Query Match 88.9%; Score 986.4; DB 7; Length 1056;
Best Local Similarity 99.4%; Pred. No. 1.8e-301;
Matches 990; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 115 TTGGTAGTCACTGAAACAATTTCTGTATTAACAGGTCCCAAGGCTTATCTGACTACG 174
Db 61 TCTGCTGTGTCAGTGAACAATTTCTGTATTAACAGGTCCCAAGGCTTATCTGACTACG 120
Qy 175 ACTAGTGTGGCTTGGTGGGCGGAGAGTGGCATGAGAGTGCAGAGTTCAGTTGGCTGG 234
Db 121 ACTAGTGTGGCTTGGTGGGCGGAGAGTGGCATGAGAGTGCAGAGTTCAGTTGGCTGG 180
Qy 235 GAAGCTGGAACCTGCGCTGAAATGCTCTTCAAGCTTCCACCAACAGGCTGAGAGT 294
Db 181 GAAGCTGGAACCTGCGCTGAAATGCTCTTCAAGCTTCCACCAACAGGCTGAGAGT 240
Qy 295 GCTACCAAGAGACTTCTCTATACATGCTATACAGCTTCTGAGATCATATCATATC 354
Db 241 GCTACCAAGAGACTTCTCTATACATGCTATACAGCTTCTGAGATCATATCATATC 300
Qy 355 ACCAAGAACTTACATAGGCTGACTTGGAAACCTGCTGTGATGGGTCAACAAATGA 414
Db 301 ACCAAGAACTTACATAGGCTGACTTGGAAACCTGCTGTGATGGGTCAACAAATGA 360
Qy 415 AAAACAGAGGCGCATGCTGATCTGGGAGGCTGACGCAATATGTGAATTTGGGGA 474
Db 361 AAAACAGAGGCGCATGCTGATCTGGGAGGCTGACGCAATATGTGAATTTGGGGA 420
Qy 475 AGGATCTTCAAACTTTTGTGAGCAAGTTTGAAGAGGGAAGATGCCAGGCTGTATG 534
Db 421 AGGATCTTCAAACTTTTGTGAGCAAGTTTGAAGAGGGAAGATGCCAGGCTGTATG 480
Qy 535 AATCTTCAACAAAGAGGCGGAGAGCTGCAAGTGAAGGCAATGAAAGGCAATGC 594
Db 481 AATCTTCAACAAAGAGGCGGAGAGCTGCAAGTGAAGGCAATGAAAGGCAATGC 540
Qy 595 AATGTGATGAGCTCTGTGGAGCTGCAGCATACAGATGTGGCTGAGCTGAGTAA 654
Db 541 AATGTGATGAGCTCTGTGGAGCTGCAGCATACAGATGTGGCTGAGCTGAGTAA 600
Qy 655 TTCCGGAGATGGAGACTTAAAGGCAAGTATGACAGGCGCTGAAAAATTGAATG 714
Db 601 TTCCGGAGATGGAGACTTAAAGGCAAGTATGACAGGCGCTGAAAAATTGAATG 660
Qy 715 GATTAAGCGGCGAGCTGAGAGCTGGGAAACAGCGCGGAGGCGCACTGGGTGCCGCTGAGGCC 774
Db 661 GATTAAGCGGCGAGCTGAGAGCTGGGAAACAGCGCGGAGGCGCACTGGGTGCCGCTGAGGCC 720
Qy 775 TTCCCTCTAGCGAGAGGCGGAGCTGATCTTTTAAAGAAATCAACAGATTACTGTACC 834
Db 721 TTCCCTCTAGCGAGAGGCGGAGCTGATCTTTTAAAGAAATCAACAGATTACTGTACC 780
Qy 835 TGCATTTCCAGCTTGGGAGCTGATGAGCAAGAGGCTGAGTGGCTTACAGAAACAGCCAC 894
Db 781 TGCATTTCCAGCTTGGGAGCTGATGAGCAAGAGGCTGAGTGGCTTACAGAAACAGCCAC 840
Qy 895 AACACATCCAGTGGGAGCGAGCTGAGTGGGCGGCTGTGATGAGTGGTGGGCTGAG 954
Db 841 AACACATCCAGTGGGAGCGAGCTGAGTGGGCGGCTGTGATGAGTGGTGGGCTGAG 900
Qy 955 GTGGAAGAGAGGAAATGAGGTGATTAAGCAGCTGTAATTCAGTGGTGGTGT 1014
Db 901 GTGGAAGAGAGGAAATGAGGTGATTAAGCAGCTGTAATTCAGTGGTGGTGT 960
Qy 1015 ACGGTCAAGTGTGACAGTGTAGGAGTGTGTGAGCAAGTATTACTGGCGACGCTCCCA 1074

QY 726 GCTGAGACCTGGAAACAGGCGCGACCTGGTGGCCCTGAGGCTTCTTCTAG 785
Db 721 GCCGCTGCGGACGCCACCTTCTGCGCATCAACAGCTGGCAG--CTATCAGAACCC 788
QY 786 CGCAGAGCGGAACTGATCTTTTATAGAAATACACAGATTACTGTACCTGAATTCCAG 845
Db 789 CATGAGACAGACCTGGTGTACATTGAGAAAGTGGCCAACTACTCGAGAGAGAGCGGCG 848
QY 846 CCTGGCATCTATGSCACAGAGGTGCTGAGTGCCTTACAGAAACAGCCACATCCAG 905
Db 849 CACGGGCGACCGTGGGSCACGAGGGCCGTCTCTGCAACCGCACGTGGCCCGGCGGAGCG 908
QY 906 GTGGAGCGACGTAGCTGTGGCG 929
Db 909 CTGTGACACCATGTGTCTGGCGCG 932

RESULT 5

US-10-364-888-1

; Sequence 1, Application US/10364888

; GENERAL INFORMATION:

; APPLICANT: Rastelli, Luca

; APPLICANT: Zhong, Haihong

; APPLICANT: Boldog, Ferenc

; APPLICANT: Gangolli, Esha

; APPLICANT: Guo, Xiaojia

; APPLICANT: Malyankar, Uriel

; APPLICANT: Pattnayak, Meera

; APPLICANT: Pena, Carol

; APPLICANT: Shimkets, Richard

; APPLICANT: Splyek, Kimberly

; APPLICANT: Vernet, Corine

; APPLICANT: Rieger, Daniel

; APPLICANT: Edinger, Shlomit

; APPLICANT: Burgess, Catherine

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 15966-744CIP

; CURRENT APPLICATION NUMBER: US/10/364,888

; CURRENT FILING DATE: 2003-02-12

; PRIOR APPLICATION NUMBER: 60/356,375

; PRIOR FILING DATE: 2002-02-12

; PRIOR APPLICATION NUMBER: 60/387,082

; PRIOR FILING DATE: 2002-06-07

; PRIOR APPLICATION NUMBER: 09/625,634

; PRIOR FILING DATE: 2000-07-26

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: CursSeqList version 0.1

; SEQ ID NO 1

; LENGTH: 1047

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1047)

; US-10-364-888-1

Query Match 14.8%; Score 164.4; DB 7; Length 1047;

Best Local Similarity 54.0%; Pred. No. 4.9e-41; Mismatches 336; Indels 6; Gaps 3;

Matches 402; Conservative 0; Mismatches 336; Indels 6; Gaps 3;

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Db 192 GGGGGCGCAGATGGGATCAAGAGTGCAGTTCGCTTGGAGCGTGAATG 251
QY 249 CCTGAAAATGCTTTCAGCTTCCACCACCAACAGGCTGAGAGTGTCTACAGAGAC 308
Db 252 CTCTCCCTCGCGAGAGACGCTTTCGGGCAAGGCTCCAGTAGGAGCGCTGAGAGC 311
QY 309 TTCCTTCAATAGTATGATGCTGCTGGAGTCAATGATCAATCAACAGAACTAG 368
Db 312 TGCCTTCAGTAGAGCATACCGGCGCTGGCGGACCGCGTACCGCTGCGAG 371
QY 369 CATGGTGAATTCGAAAATGTGTGCTGTGATGGTCAAAATAG---AAAAACAGAGG 425

Db 372 CCAAGGAACCTGAGCACTGCGGCTGGACCGGAGAGCAGGCTACTCAACCAAGC 431
QY 426 CCATGGCTGATCTGGGAGGCTGACGAGCAATGTGAAATTTGGGAAAGATCTCCAA 485
Db 432 CGAGGCTGGAATGTGGGCGGCTGCTGGCCGAGCTGTGTTACGACATGACTTCTCCG 491
QY 486 ACTCTTGTGACAGTTTGAAGAGGAGATGCCAGAGCCTTGATGAATCTTCAAA 545
Db 492 GCGCTTGATGACCTGCGGAGATCAAGAGAACGCGGCGGCTCATGAATCTGCAATA 551
QY 546 CAAAGGCGCGGACAGCTGCGAGTGAAGACCAATGAAAGACATCCAAATGATNG 605
Db 552 CAATGAGGCGCGCAGAAAGTCTTGAAGACCGATGAGCTGAGTGAAGTCCACAGG 611
QY 606 CATCTTGGAGCTGACAGATACAGACATGCTGCTGCTGCTGATTCGGGAGAT 665
Db 612 GGTCTGTGCTCTGACACCAACCAAACTGCTGACACAGCTGCCAAGTTCCAGAGGT 671
QY 666 GGGAGACTACTTAAAGCCAAATATGACCAAGCGCTGAAAATTGAATGATAAGCGCA 725
Db 672 GGGGCACTGCTGAAGAGAAAGTACAAAGCGGCGGTGAGTGAAGTGG--TGCGGGCCA 730
QY 726 GCTGAGACTTGGAAACAGCGCCGAGGGCACTGGGTGCCCTGAGGCTTCTTCTTAG 785
Db 731 GCCGCTGCGGACGCCCACTTCTGCGCATCAACAGCTGCGAG--CTATCAGAAAGCC 788
QY 786 CGCAGAGCGGACATGATCTTTTAAAGGATCAACGATTAATCTGATCCCAATTCAG 845
Db 789 CATGAGACAGACCTGCTGATGATTAAGAAATGCGCCCACTACTTGCAGAGAGACCGGC 848
QY 846 CCTGGCATCTATGSCACAGAGGTGCTGAGTGCCTTACAGAAACCAACATCCAG 905
Db 849 CACGGGCGACGCTGGGCAACGAGGCGCGTCTGCAACCGCACGTGCGCGCGGAGCG 908
QY 906 GTGGAGCGACGTAGCTGTGGCG 929
Db 909 CTGTGACACCATGTGTCTGGCGCG 932

RESULT 6

PCT-US03-04188-7

; Sequence 7, Application PC/TUS0304188

; GENERAL INFORMATION:

; APPLICANT: Curagen Corporation, et al

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 15966-744CIP PCT

; CURRENT APPLICATION NUMBER: PCT/US03/04188

; CURRENT FILING DATE: 2003-02-12

; PRIOR APPLICATION NUMBER: 60/356,375

; PRIOR FILING DATE: 2002-02-12

; PRIOR APPLICATION NUMBER: 60/387,082

; PRIOR FILING DATE: 2002-06-07

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: CursSeqList version 0.1

; SEQ ID NO 7

; LENGTH: 2160

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (6)..(1052)

; PCT-US03-04188-7

Query Match 14.8%; Score 164.4; DB 1; Length 2160;

Best Local Similarity 54.0%; Pred. No. 6.8e-41; Mismatches 336; Indels 6; Gaps 3;

Matches 402; Conservative 0; Mismatches 336; Indels 6; Gaps 3;

QY 189 GGGTCCCAAGATGCGATCGAGAGTGCAGTTGCTTGGGAACGCTGGAATG 248
Db 197 GGGGGCGCAGATGGGATCAAGAGTGCAGTTCGCTTGGAGCGTGAATG 256
QY 249 CCTGAAAATGCTTTCAGCTTCCACCACCAACAGGCTGAGAGTGTCTACAGAGAC 308

GenCore version 5.1.6
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OW protein - protein search, using BW model

Run on: January 30, 2004, 13:22:49 ; Search time 44 Seconds

(without alignments)
1331.139 Million cell updates/sec

Title: US-09-898-456-7

Perfect score: 2037
Sequence: 1 MLCCICQCLVSPPTLTPC.....SKYYCARSPGSAQSLGKNSA 369

Scoring table: BLASTN62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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21: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1808	88.8	351	23	Human wingless-lik
2	1804	88.6	351	23	Novel human protei
3	1802	88.5	351	23	MO4 protein sequ
4	1783	87.5	415	22	Human Wnt3 (Zmnc3)
5	1779	87.3	415	24	Human wingnut prot
6	1496	73.4	354	22	Human Wnt-8B prot
7	1213	59.5	351	22	Novel human diagno
8	1213	59.5	351	24	WNT-8B protein. U
9	1213	59.5	351	24	Human WNT-8B prot

10	1137.5	55.8	295	22	AAE02909
11	654.5	32.1	380	23	AAU85413
12	649.5	31.9	359	21	AAV57271
13	649.5	31.9	359	23	ABG61843
14	649.5	31.9	372	24	AAE34040
15	649.5	31.9	372	24	ABU55884
16	649.5	31.9	372	24	ABU07452
17	648	31.8	351	20	AAV41719
18	648	31.8	351	21	AAE44275
19	648	31.8	351	21	AAV57270
20	648	31.8	351	21	AAV57273
21	648	31.8	351	22	AAU29063
22	648	31.8	351	22	AAU38889
23	648	31.8	351	24	ABU71151
24	648	31.8	351	24	ABU65608
25	648	31.8	351	24	ABU65941
26	648	31.8	351	24	ABU67445
27	648	31.8	351	24	ABU61105
28	648	31.8	351	24	ABU65303
29	648	31.8	351	24	ABU58439
30	648	31.8	351	24	ABU55975
31	648	31.8	351	24	ABU6970
32	648	31.8	351	24	ABU10549
33	648	31.8	365	22	AAU40675
34	648	31.8	365	22	AAE09707
35	640.5	31.4	360	21	AAV70734
36	640.5	31.4	360	21	AAV57595
37	640.5	31.4	360	24	AAE34039
38	640.5	31.4	360	24	ABU55883
39	637	31.3	370	21	ABU19786
40	636.5	31.2	365	21	AAV70739
41	636.5	31.2	365	21	AAV57600
42	636.5	31.2	365	22	AAE73619
43	636.5	31.2	365	23	AAU65414
44	636.5	31.2	365	24	AAE34041
45	636.5	31.2	365	24	ABP58342

ALIGNMENTS

RESULT 1	
AAU47902	AAU47902 standard; Protein; 351 AA.
ID	
AC	AAU47902;
XX	
DT	25-FEB-2002 (first entry)
XX	
DE	Human wingless-like Wnt-8D seq ID NO 2.
XX	
KW	Human; wingless-like gene; Wnt-8D, antistimatic; nocotropic; vaccine;
KW	neuroprotective; cytosolic; antidepressant; neuroleptic; vasotrophic;
KW	cardioprotective; vulnary; aschma; Alzheimer's disease; cancer;
KW	cardiomyopathy; depression; schizophrenia; ischaemia; stroke;
KW	wound healing; kidney disease; lung disorder; apoptosis;
KW	stem cell therapy; immunological response; gene therapy.
XX	
OS	Homo sapiens.
XX	
PN	WO200183543-A1.
XX	
PD	08-NOV-2001.
XX	
PF	30-APR-2001; 2001WO-EP04887.
XX	
PR	03-MAY-2000; 2000EP-0109422.
XX	
PA	(MERE) MERCK PATENT GMBH.
XX	
FI	Duecker K;
XX	
DR	WPI; 2002-034504/04.

Human Wnt-8B prote
Human protein NOV1
Wnt-4AF and Wnt-5c
Prostate cancer-as
WNT-2B protein. U
Human WNT-2B prot
Protein differentl
Human PRO864 prote
Human PRO864 (UNQ4
Wnt-4AF and Wnt-5c
Wnt-4AF and Wnt-5c
Human PRO polypept
Human polypeptide
Human PRO864 prote
Human secreted/cra
Novel human secret
Human secreted/cra
Human PRO864 polyp
Human PRO polypept
Human PRO polypept
Human secreted/cra
Human PRO polypept
Human secreted/cra
Human gene 3 encod
Human Wnt-2 protei
Human Wnt-2 protei
WNT-2 protein. Un
Human WNT-2 prote
Human Wnt-1 protei
Human Wnt-5a prote
Human Wnt-5a prote
Wnt-5a tumour supp
Human protein NOV1
WNT-4 protein. Un
Human cell growth,

DR N-PSDB; ABA05327.
 XX New wingless/int 8D polypeptide, useful for treating asthma,
 PT Alzheimer's disease, cancer, ischaemia, stroke, depression,
 PT schizophrenia, aberrant apoptosis and for identifying modulators of
 XX polypeptide activity
 PS Claim 4; Page 37-38; 43pp; English.
 XX
 CC The invention relates to a polypeptide (I) having a fully defined
 CC wingless/int 8D (Wnt-8D) protein sequence of 351 amino acids (AAW4/902)
 CC or is encoded by a defined polynucleotide sequence (II) of 1650
 CC nucleotides (ABA05327) or is a polypeptide having 95% identity to (I) or
 CC fragments or variants of above mentioned polypeptides. (I) has
 CC antitastmatic, neurotropic, neuroprotective, cytosolic, antidepressant,
 CC neuroleptic, vasotropic, cerebroprotective and vulnerary activity. (I) is
 CC useful for identifying compounds that stimulate or inhibit the function
 CC or level of the polypeptide. (I) and (II) are useful for treating asthma,
 CC Alzheimer's disease, cancer, cardiomyopathies, depression, schizophrenia,
 CC general psychotic disorders, ischaemia, stroke, wound healing, kidney
 CC diseases, lung disorders, aberrant apoptosis, tissue remodeling, stem
 CC cell therapies. (I) and (II) are also useful as vaccines for inducing an
 CC immunological response in a mammal and in gene therapy.
 XX
 SQ Sequence 351 AA;
 Query Match 88.8%; Score 1808; DB 23; Length 351;
 Best Local Similarity 98.2%; Pred. No. 6, 2e-163;
 Matches 331; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 33 CLTFLSFRSVNNFLITGPKAVLYTTSVALGAOSGIECKFOFAMERNCPENALQIST 92
 DB 15 CAFSASMSVNNFLITGPKAVLYTTSVALGAOSGIECKFOFAMERNCPENALQIST 74
 QY 93 HNRLSATRETFRIHAISAGVWYITTKNCSMGDFENCCDGSNNKTCGHCIMWGCS 152
 DB 75 HNRLSATRETFRIHAISAGVWYITTKNCSMGDFENCCDGSNNKTCGHCIMWGCS 134
 QY 153 NVEFGERSKLFVDSLEKGDARALMNLNRRAGRAVATMKRTCKGHSIGSGSIOTC 212
 DB 135 NVEFGERSKLFVDSLEKGDARALMNLNRRAGRAVATMKRTCKGHSIGSGSIOTC 194
 QY 213 WQLAEFRMGDYLKAKYDQALKIEMDKQLRAGNSAEGHWPAEAFLPSAAELIPLFE 272
 DB 195 WQLAEFRMGDYLKAKYDQALKIEMDKQLRAGNSAEGHWPAEAFLPSAAELIPLFE 254
 QY 273 SPDYCTCNSSLDGIYGTGREGCLQNSHNTRSRWRSSCGRLCTECGLQVERKEVTISSCNC 332
 DB 255 SPDYCTCNSSLDGIYGTGREGCLQNSHNTRSRWRSSCGRLCTECGLQVERKEVTISSCNC 314
 QY 333 KFOWCCTVCKDQCRHVSKYVGCARSPGSAOSIGKGA 369
 DB 315 KFOWCCTVCKDQCRHVSKYVGCARSPGSAOSIGKGA 351

RESULT 2
 ABB60975
 ID ABB60975 standard; Protein; 351 AA.
 XX ABB60975;
 AC 10-SEP-2002 (first entry)
 XX
 DT Novel human protein. SEQ ID 62.
 DE
 XX
 XX Human; cytosolic; vulnerary; antiarteriosclerotic; antiparkinsonian;
 KM neurotropic; neuroprotective; immunosuppressive; haemostatic;
 KM antiinflammatory; cardiact; antitumor; virucide; antithyroid;
 KM cerebroprotective; anorectic; metabolic; vaccines; cancer; infection;
 KM wound healing disorders; atherosclerosis; Parkinson's disease;
 KM Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
 KM inflammation; neoplastic disease; nervous system disorder;
 KM cardiovascular disorders; pancreatitis; respiratory disorder;

KM hyperproliferation; systemic autoimmune disease; hyper-immunity;
 KM developmental abnormality; gastrointestinal ulceration; neuropathy;
 KM haematological disease; metabolic diseases; sperm dysfunction;
 KM thyroid disorder; hypothyroidism; brain damage; colitis;
 KM come photo- transduction deficiency; neurological disease; stroke;
 KM angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
 KM trachea; thymus; lymph node; muscular system; obesity; anorexia;
 KM growth abnormality; precocious puberty.
 XX
 OS Homo sapiens.
 XX
 XX WO200250105-A1.
 PN 27-JUN-2002.
 XX
 PF 17-DEC-2001; 2001WO-US49232.
 XX
 XX 19-DEC-2000; 2000US-256710P.
 PR 20-DEC-2000; 2000US-257048P.
 PR 09-JAN-2001; 2001US-260482P.
 PR 30-JAN-2001; 2001US-264922P.
 PR 06-FEB-2001; 2001US-266797P.
 PR 19-MAR-2001; 2001US-276989P.
 PR 04-APR-2001; 2001US-281535P.
 PR 08-MAY-2001; 2001US-289622P.
 XX
 PA (SMTK) SMTHTLINE BECHAM CORP.
 PA (SMTK) SMTHTLINE BECHAM PLC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Agarwal P, Birkeland M, Cogswell JP, Kabnick KE, Lai Y;
 PI Marenson SA, Rizvi SK, Smith RF, Strum JC, Xie Q;
 XX MPI. 2002-508784/54.
 DR N-PSDB; ABB60975.
 XX
 PT Secreted proteins and polynucleotides useful as vaccines for preventing
 PT or treating various diseases e.g. cancer, wounds, atherosclerosis,
 PT Parkinson's disease, Alzheimer's disease, infection, autoimmune
 PT disorder
 XX
 PS Claim 1(a); Page 267-268; 335pp; English.
 XX
 CC The invention relates to an isolated polypeptide with signal sequences
 CC which allow it to be secreted extracellularly or membrane associated.
 CC The activity of polypeptides of the invention may be described as,
 CC cytosolic, vulnerary, antiarteriosclerotic, antiparkinsonian, neurotropic,
 CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory,
 CC cardiact, antitumor, virucide, antithyroid, cerebroprotective, anorectic,
 CC and metabolic. Polypeptides and polynucleotides of the invention are
 CC useful in the treatment, or as a vaccine in the prevention of, cancer,
 CC wound healing disorders, infection, atherosclerosis, Parkinson's disease
 CC and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,
 CC inflammation, neoplastic diseases, nervous system related disorders and
 CC cardiovascular disorders, pancreatitis, respiratory disorder.
 CC hyperproliferation, systemic autoimmune disease, hyper-immunity,
 CC developmental abnormality, gastrointestinal ulceration, neuropathy,
 CC haematological diseases, metabolic diseases, sperm dysfunction, thyroid
 CC disorders e.g. hypothyroidism, brain damage, colitis, cone photo-
 CC transduction deficiency, neurological diseases, stroke, angiogenesis,
 CC ovulation disorders, diseases in the spinal cord, thyroid gland, heart,
 CC trachea, thymus, lymph node and muscular system, obesity, anorexia,
 CC growth abnormalities, and alleviation of precocious puberty. The
 CC sequences given in records ABB60965-ABB61019 represent novel human
 CC proteins of the invention.
 XX
 SQ Sequence 351 AA;
 Query Match 88.6%; Score 1804; DB 23; Length 351;
 Best Local Similarity 97.9%; Pred. No. 1, 5e-162;
 Matches 330; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 33 CLTFLSFRSVNNFLITGPKAVLYTTSVALGAOSGIECKFOFAMERNCPENALQIST 92


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Db      15 CAAFSASAMSVNNFLITGPAYLYTTYSVALGAQSGIEECKFPAMERNPCPENALQLST 74
Qy      93 HNLRSATRETSFTHAISSAGVWYITTKNSMGDFENCGDGSNNKGTHGHWGSCSD 152
      75 HNLRSATRETSFTHAISSAGVWYITTKNSMGDFENCGDGSNNKGTHGHWGSCSD 134
Db      153 NVEFGERISKLFDLSLEKGDARALMNLHNNRAGRLAVRAMTKCTCKHGISGSCSIQTC 212
      135 NVEGERISLFLVDSLEKGDARALMNLHNNRAGRLAVRAMTKCTCKHGISGSCSIQTC 194
Qy      213 WLQLAEREMGDYKAKYDQALKIEMDKROLRAGNSAEGHWVPAEALPSEAEELIFLEE 272
      195 WLQLAEREMGDYKAKYDQALKIEMDKROLRAGNSAEGHWVPAEALPSEAEELIFLEE 254
Qy      273 SPDYCTCNSSLGIYGTGREGCLONSHNTSRWERSGRLCTEGGLQYERKTEVISSCNC 332
      255 SPDYCTCNSSLGIYGTGREGCLONSHNTSRWERSGRLCTEGGLQYERKTEVISSCNC 314
Db      333 KFWCCTVCKDCQCRHVSKYKCARSPSAQSLGKGS 369
      315 KFWCCTVCKDCQCRHVSKYKCARSPSAQSLGKGS 351

RESULT 3
AAM47662 standard; Protein: 351 AA.
XX      AAM47662;
XX      21-FEB-2002 (first entry)
XX      MOLA protein sequence.
XX      MOLA; G-coupled protein-receptor; cardiomyopathy; atherosclerosis;
XX      cell signal processing; metabolic disorder; diabetes; cancer;
XX      neurodegenerative disorder; immune disorder; cardiac disorder;
XX      lung disease; autoimmune disease; developmental disorder; anti-diabetic;
XX      cytotoxic; Neuroprotective; Antiatherosclerotic; Immunosuppressive;
XX      Gene therapy; Vaccine; anti-inflammatory; MOLA;
XX      Mnt 8-like protein.
XX      Unidentified.
XX      W0200181578-A2.
XX      01-NOV-2001.
XX      26-APR-2001; 2001WO-US13578.
XX      26-APR-2000; 2000US-200158P.
XX      28-APR-2000; 2000US-200613P.
XX      28-APR-2000; 2000US-200780P.
XX      01-MAY-2000; 2000US-201006P.
XX      01-MAY-2000; 2000US-201007P.
XX      01-MAY-2000; 2000US-201236P.
XX      01-MAY-2000; 2000US-201238P.
XX      02-MAY-2000; 2000US-201186P.
XX      03-MAY-2000; 2000US-201474P.
XX      03-MAY-2000; 2000US-201508P.
XX      25-JUL-2000; 2000US-2020591P.
XX      15-SEP-2000; 2000US-233678P.
XX      22-JAN-2001; 2000US-263217P.
XX      30-JAN-2001; 2001US-265160P.
XX      (CURA-) CURAGEN CORP.
XX      Vernet CM, Fernandes ER, Gerlach V, Shinkens RA, Malyankar UM,
XX      Boldog FL, Zernusen BP, Spyrek KA, Majumder K, Tchernev VT,
XX      Padigaru M, Paccutajan M, Burgess CE, Gangoli EA, Smithson G,
XX      Rastelli L, MacDougall JR, Taupier RJ, Grose WM, Szekeres ES,
XX      Alsbrook JP,
XX

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DR      WPI, 2002-049278/06.
XX      N-PSDB; ABA04592.
XX      Novel G-protein coupled receptor-related polypeptides and
PT      polynucleotides for diagnosing, preventing and treating cardiomyopathy,
PT      atherosclerosis, disorders related to cell signal processing and for
PT      identifying modulators
XX      Claim 1; Page 34; 227bp; English.
XX      The present invention relates to novel G-coupled protein-receptor related
CC      proteins and coding sequences (MOLA, where X is a number from 1 to 10,
CC      ABA04589-ABA04603 and AAM47659-AAM47673). MOLA proteins and coding
CC      sequences are useful for treating or preventing a MOLA-associated
CC      disorder, such as cardiomyopathy, atherosclerosis, disorders related to
CC      cell signal processing and metabolic pathway modulation, diabetes and
CC      cancer. Additionally, MOLA proteins and coding sequences are useful for
CC      preventing and treating a variety of disorders including metabolic
CC      disorders, nutritional oedema, chronic and hereditary pancreatitis,
CC      obesity, infectious disease, anorexia, neurodegenerative disorders,
CC      Alzheimer's disease, Parkinson's disease, stroke, immune disorders,
CC      hematopoietic disorders and various dyslipidaemias, metabolic syndrome X
CC      and wasting disorders associated with chronic diseases and cancers,
CC      cardiac disorders, hypertension, hypercalcaemia, cirrhosis, angiogenesis
CC      and wound healing, trauma, glomerulonephritis, hyper and hypothyroidism,
CC      multiple sclerosis, lung diseases including asthma, Crohn's disease,
CC      scleroderma, autoimmune diseases, developmental disorders and neural tube
CC      defects. The present sequence is the protein sequence for MOLA.
CC      MOLA is a Mnt 8-like protein.
XX      SQ      Sequence 351 AA;
XX      Query Match 88.5%; Score 1802; DB 23; Length 351;
XX      Best Local Similarity 97.9%; Pred. No. 2,3e-162;
XX      Matches 330; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy      33 CLTFSLFGRSVNNFLITGPAYLYTTYSVALGAQSGIEECKFPAMERNPCPENALQLST 92
      15 CAAFSASAMSVNNFLITGPAYLYTTYSVALGAQSGIEECKFPAMERNPCPENALQLST 74
Db      93 HNLRSATRETSFTHAISSAGVWYITTKNSMGDFENCGDGSNNKGTHGHWGSCSD 152
      75 HNLRSATRETSFTHAISSAGVWYITTKNSMGDFENCGDGSNNKGTHGHWGSCSD 134
Qy      153 NVEFGERISKLFDLSLEKGDARALMNLHNNRAGRLAVRAMTKCTCKHGISGSCSIQTC 212
      135 NVEGERISKLFDLSLEKGDARALMNLHNNRAGRLAVRAMTKCTCKHGISGSCSIQTC 194
Db      213 WLQLAEREMGDYKAKYDQALKIEMDKROLRAGNSAEGHWVPAEALPSEAEELIFLEE 272
      195 WLQLAEREMGDYKAKYDQALKIEMDKROLRAGNSAEGHWVPAEALPSEAEELIFLEE 254
Qy      273 SPDYCTCNSSLGIYGTGREGCLONSHNTSRWERSGRLCTEGGLQYERKTEVISSCNC 332
      255 SPDYCTCNSSLGIYGTGREGCLONSHNTSRWERSGRLCTEGGLQYERKTEVISSCNC 314
Qy      333 KFWCCTVCKDCQCRHVSKYKCARSPSAQSLGKGS 369
      315 KFWCCTVCKDCQCRHVSKYKCARSPSAQSLGKGS 351
Db      315 KFWCCTVCKDCQCRHVSKYKCARSPSAQSLGKGS 351

RESULT 4
AAB02906 standard; Protein: 415 AA.
XX      AAB02906;
XX      10-AUG-2001 (first entry)
XX      Human Wnt3 (Zmwt3) protein.
XX      Human Wnt3 (Zmwt3) protein.
XX      Human Wnt3; gene therapy; cellular signalling; education tool;
XX      tissue development; biopharmaceutical; antibody production; glycoprotein.
XX

```

```
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Key difference 171
FT /note= "Encoded by GTC"
XX
XX WO200138353-A2.
XX
XX 31-MAY-2001.
XX
XX 17-NOV-2000; 2000WO-US31820.
XX
XX 22-NOV-1999; 99US-0444788.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Holloway JL;
XX
XX WPI; 2001-367660/38.
XX
XX N-PSDB; AAD06571.
XX
XX Zmwnt3 polypeptides useful for producing antibodies, for
XX biopharmaceuticals, and as educational tools in laboratory practical
XX kits.
XX
XX Claim 1; Page 3; 82pp; English.
XX
XX The present sequence is human Wnt3 (Zmwnt3) protein which is a
XX cellular signalling molecule. Wnt proteins are a family of secreted
XX glycoproteins, which, in many organisms, have a role in morphological
XX development of tissues in both embryonic and adult contexts. Wnt3 DNA
XX and protein are useful as education tools in laboratory practical kits
XX for genetics and molecular biology, protein chemistry and antibody
XX production, and analysis. Wnt3 protein is useful as an aid to teach
XX preparation of antibodies, identify proteins by Western blotting,
XX protein purification, determining the weight of expressed Zmwnt3
XX polypeptides as a ratio of total protein expressed, identifying peptide
XX cleavage sites, coupling amino acids and carboxyl terminal tags, amino
XX acid sequence analysis and monitoring biological activities of both
XX native and tagged protein in vitro and in vivo. Ab is useful for
XX purifying Zmwnt3, and cloning and sequencing the polynucleotides that
XX encode an antibody, hence in the design of humanised antibodies.
XX Wnt3 DNA is also useful in gene therapy.
XX
XX Sequence 415 AA:
XX
XX Query Match 87.5%; Score 1783; DB 22; Length 415;
XX Best Local Similarity 98.2%; Pred. No. 1.8e-160;
XX Matches 326; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX 33 CLTFLPGRSVNNPILITGPKAVLTITTSVALGAOSGIECKPQFMRWNCPENALQST 92
XX 15 CAAFASASWVNNPILITGPKAVLTITTSVALGAOSGIECKPQFMRWNCPENALQST 74
XX
XX 93 HNRRLSATRETSFIHAISAGVMIITKNCSGKDPENCGCGSNNKGTGHWIGGCS 152
XX 75 HNRRLSATRETSFIHAISAGVMIITKNCSGKDPENCGCGSNNKGTGHWIGGCS 134
XX
XX 153 NVEFGERISKLFVDSLEKGDARALMNIHNNRAGLAVPATMKRTCKHGISGCSITC 212
XX 135 NVEFGERISKLFVDSLEKGDARALMNIHNNRAGLAVPATMKRTCKHGISGCSITC 194
XX
XX 213 WLQALAEFRMGDYLAKYDQALKIMDKROLRAGSASGHWVPAFLPSAEELIFLEE 272
XX 195 WLQALAEFRMGDYLAKYDQALKIMDKROLRAGSASGHWVPAFLPSAEELIFLEE 254
XX
XX 273 SPDYCTNSSLIGIYETEGRECLQNSHTSRWRERSCGLTECGIQLVERERTEVSSGNC 332
XX 255 SPDYCTNSSLIGIYETEGRECLQNSHTSRWRERSCGLTECGIQLVERERTEVSSGNC 314
XX
XX 333 KFWMCCTVKKDQCRHVVSKYYCARSPGSAQSL 364
XX
```

```
DB 315 KFWMCCTVKKDQCRHVVSKYYCARSPGSAQSL 346
XX
XX RESULT 5
XX ABG72362
XX ID ABG72362 standard; Protein: 415 AA.
XX
XX ABG72362;
XX
XX 07-FEB-2003 (first entry)
XX
XX Human wingnut protein Zmwnt3.
XX
XX Human; wingnut; Zmwnt3; signalling molecule; secreted glycoprotein;
XX extracellular matrix; tumour; brain development.
XX
XX Homo sapiens.
XX
XX Location/Qualifiers
XX Key 30..42
XX Peptide /note= "This peptide is claimed in claim 5"
XX Peptide 44..62
XX Peptide /note= "This peptide is claimed in claim 4"
XX Peptide 69..97
XX Peptide /note= "This peptide is claimed in claim 4"
XX Peptide 101..111
XX Peptide /note= "This peptide is claimed in claim 5"
XX Peptide 120..138
XX Peptide /note= "This peptide is claimed in claim 4"
XX Peptide 143..177
XX Peptide /note= "This peptide is claimed in claim 4"
XX Peptide 184..215
XX Peptide /note= "This peptide is claimed in claim 4"
XX Peptide 217..231
XX Peptide /note= "This peptide is claimed in claim 4"
XX Peptide 217..248
XX Peptide /note= "This peptide is claimed in claim 4"
XX Peptide 231..248
XX Peptide /note= "This peptide is claimed in claim 4"
XX Peptide 276..297
XX Peptide /note= "This peptide is claimed in claim 4"
XX Peptide 321..345
XX Peptide /note= "This peptide is claimed in claim 4"
XX Peptide 345..415
XX Peptide /note= "This peptide is claimed in claim 4"
XX
XX US2002123103-A1.
XX
XX 05-SEP-2002.
XX
XX 03-DEC-2001; 2001US-0005947.
XX
XX 22-NOV-1999; 99US-166827P.
XX 17-NOV-2000; 2000US-0715993.
XX
XX (HOLL/) HOLLOWAY J L.
XX
XX Holloway JL;
XX
XX WPI; 2003-066796/06.
XX
XX N-PSDB; ABS57866.
XX
XX Novel human Zmwnt3 polypeptide useful as aid for identifying proteins by
XX Western blotting, to teach analytical skills such as mass spectrometry
XX and circular dichroism, and for identifying peptide cleavage sites -
XX
XX Claim 3; Page 2; 37pp; English.
XX
XX The invention relates to an isolated human Zmwnt3 polypeptide (a wingnut
XX protein which is a signalling molecule/secreted glycoprotein, found
XX in the extracellular matrix) that is at least 80% identical to
XX the protein appearing as ABG72362 sequence (S1) of 415 amino acids,
XX where the polypeptide specifically binds with an anti-Zmwnt3
XX
```

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OM protein - protein search, using sw model

Run on: January 30, 2004, 13:27:05 ; Search time 20 Seconds
(without alignments)
1774.312 Million cell updates/sec

Title: US-09-898-456-7
Perfect score: 2037
Sequence: 1 MLCICQLCLVSPFPTLTPC.....SKYYCARSGAQLGKSA 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1388	68.1	387	2	developmental regu
2	1379	67.7	357	2	wnt-8c - chicken
3	1287.5	63.2	361	2	gene wnt8 protein
4	1215.5	59.7	358	2	gene wnt8b protein
5	1155	56.7	428	2	Xwnt-8b - African
6	672.5	33.0	360	2	wnt-5c protein - A
7	659	32.4	352	2	developmental regu
8	656.5	32.2	359	2	cell-cell signalin
9	655.5	32.2	357	2	cell-cell signalin
10	652.5	32.0	370	2	wnt-1 protein - ze
11	649.5	31.9	372	2	secreted glycoprot
12	644	31.6	351	2	wnt-4 protein - mo
13	643.5	31.6	360	2	wnt-2 protein - mo
14	640.5	31.4	369	2	wnt-1-like protein
15	639	31.4	369	2	wnt-5b protein - m
16	638.5	31.3	372	2	proto-oncogene wnt
17	636.5	31.2	365	2	transforming prote
18	636	31.2	370	1	transforming prote
19	636	31.2	370	1	transforming prote
20	636	31.2	370	1	transforming prote
21	635	31.2	351	2	wnt-4 protein - m
22	629	30.9	351	2	wnt-3a protein - m
23	629	30.9	352	2	wnt-3 protein - mo
24	626	30.7	355	2	wnt-5a protein - m
25	623	30.6	379	2	wnt-7b protein - m
26	619.5	30.4	349	2	transforming prote
27	615.5	29.8	352	2	wnt-2 protein - fr
28	606.5	29.6	360	2	hypothetical prote
29	602.5	29.6	360	2	

30	596.5	29.3	349	2	G36470	wnt-7a protein - m
31	593	29.1	468	2	A29650	wntless (wg) prot
32	589.5	28.9	360	2	S32695	wnt-2 protein - Ca
33	589	28.9	365	2	TC7694	soluble-type glyco
34	586	28.8	364	2	F36470	wnt-6 protein - mo
35	575	28.2	348	2	TI0502	wnt-1 protein - I
36	575	28.2	372	2	S32694	wnt-1 protein - Ca
37	572.5	28.1	469	1	TVFPT1	transforming prote
38	570	28.0	398	2	T26284	hypothetical prote
39	566	27.8	333	2	A47536	gene WNT3 protein
40	557	27.3	417	2	UC7693	soluble-type glyco
41	552	27.1	417	2	B59392	wnt1a protein pro
42	551.5	27.1	354	2	UC4152	wnt-11 protein - m
43	551	27.0	442	2	IS0110	wnt1a protein pre
44	544.5	26.7	354	2	S34378	wnt-11 protein - m
45	532.5	26.1	353	2	IS1572	maternal protein -

ALIGNMENTS

RESULT 1

S18771
developmental regulator Xwnt-8 - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 22-Nov-1993 #sequence_revision 27-Oct-1995 #text_change 24-Nov-1999
C/Accession: S18771; D49764
R/Christians, J.L.; McMahon, J.A.; McMahon, A.P.; Moon, R.T.
Development 111, 1045-1055, 1991
A/Title: Xwnt-8, a Xenopus wnt-1/int-1-related gene responsive to mesoderm-inducing growth factor
A/Accession: S18771; MUID:91347916; PMID:1879349
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-387 <CHR>
A/Cross-references: EMBL:X57234
R/Christians, J.L.; Gavin, B.J.; McMahon, A.P.; Moon, R.T.
Dev. Biol. 143, 230-234, 1991
A/Title: Isolation of cDNAs partially encoding four Xenopus wnt-1/int-1-related proteins
A/Reference number: A49764; MUID:91122437; PMID:1991549
A/Accession: D49764
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 'QE', 181-242, 'T', 244-291, 'R', 293-321 <CH2>
A/Cross-references: GB:M50508
C/Superfamily: int-1 transforming protein

Query Match 68.1%; Score 1388; DB 2; Length 387;
Best Local Similarity 75.3%; Pred. No. 2e-107;
Matches 244; Conservative 40; Mismatches 40; Indels 0; Gaps 0;

QY	33	CLTFSLEGRSVNPLITGPAYLYTTYSVALGAQSGIEECKFPQAWRMNCPENALDST	92
DB	16	CPFTASAMSVNFMKMPAYLYTSASVAVGQNGIEECKYQPAWRMNCPESTLDT	75
QY	93	HNRLRSATRENSFHAISAGVWYITKNCMGDFENCGDGSNGTGGHWTGGCSD	152
DB	76	HNGIKSATRETSFVHAISAGVWYITLFRNCMGDFENCGDGSNGTGGHWTGGCSD	135
QY	153	NVEFGERISKLPVDSLEKGDARALNMLHNNRAGRLAVRAITMKTKCHGISGCSIQTC	212
DB	136	NAEFGERISKLPVDSLEKGDARALNMLHNNRAGRLAVRAITMKTKCHGISGCSIQTC	195
QY	213	WLQLAEREMGDYKAYDQALTKIEMDKRQAGNSAEHWPPEALLPSEALITLLEE	272
DB	196	WLQLAEREMGDYKAYDQALTKIEMDKRQAGNSAEHWPPEALLPSEALITLLEE	255
QY	273	SPDYCTGNSISGTYGTEGRCLONSHTSWERSRCGLCTEGCLQVEERKTEVYSSCNC	332
DB	256	SPDYCLKNISLIGLGTGRCLOSGKSLQWERRSCRCLTCLQVREKTEVYSSCNC	315
QY	333	KFOWCTVCKDCQGRHVVSKYYCAR	356

Db 316 KFMWCTVCKEQQKQVNIKHFCA 339

RESULT 2

150690

Wnt-8C - chicken

C/Species: Gallus gallus (chicken)

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C/Accession: 150690

R/Hume, C.R.; Dodd, J.

Development 119, 1147-1160, 1993

A/Title: Cmt-8C: a novel wnt gene with a potential role in primitive streak formation

A/Reference number: 150690; MUID:94139558; PMID:7916678

A/Accession: 150690

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-357 <HML>

A/Cross-references: EMBL:U02097; NID:9403577; PIDN:AA18933.1; PID:9403578

A/Genetics:

C/Supfamily: int-1 transforming protein

Query Match 67.7%; Score 1379; DB 2; Length 357;

Best Local Similarity 76.5%; Pred. No. 1e-106;

Matches 241; Conservative 37; Mismatches 37; Indels 0; Gaps 0;

42 SVNNFLITGPRAVLYTTTSVALGAQSGIECKFOFAMERNPCPNALQSTHNRISATR 101

25 SVNNFLITGPRAVLYTTTSVALGAQSGIECKFOFAMERNPCPNALQSTHNRISATR 84

102 ETSFTHAISSAGVWYITTKNSMGDFENCGDSSNNKKTGGHIMWGCSNDVEFGERIS 161

85 ETSFTHAISSAGVWYITTKNSMGDFENCGDSSNNKKTGGHIMWGCSNDVEFGERIS 144

162 KLPFDSLEKGRDARALMNLHNNRAGRLAVRAATMRTCKKIGISSCSIQTCTWLAFFRE 221

145 KLPFDSLEKGRDARALMNLHNNRAGRLAVRAATMRTCKKIGISSCSIQTCTWLAFFRE 204

222 MGDTLAKKYDQALTIEMDKRQLRAGNSAEGHWVPAEAFIPSAEALIFLESPPDYCTGNS 281

205 IGVTLKMKYDQALTIEMDKRQLRAGNSAEGHWVPAEAFIPSAEALIFLESPPDYCTGNS 264

282 SLGIYGTGEBRCLQNSHNTSRMRERSCGRLCTECGLQVEERKTEVISSCNCKFQWCTVK 341

265 SLGIYGTGEBRCLQNSHNTSRMRERSCGRLCTECGLQVEERKTEVISSCNCKFQWCTVK 324

342 CDQCRHVSXYKCAR 356

325 CEQCRQLVAKHFCAR 339

RESULT 3

150505

gene wnt8 protein - zebra fish

C/Species: Brachydanio rerio (zebra fish)

C/Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 24-Nov-1999

C/Accession: 150505

R/Kelly, G.M.; Greenstein, P.; Erezylmaz, D.F.; Moon, R.T.

Development 121, 1787-1799, 1995

A/Title: Zebrafish wnt8 and wnt8b share a common activity but are involved in distinct

A/Reference number: 150505; MUID:95324404; PMID:7600994

A/Accession: 150505

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-361 <KEL>

A/Cross-references: EMBL:U10869; NID:9968914; PID:9968915

C/Genetics:

C/Supfamily: int-1 transforming protein

Query Match 63.2%; Score 1287.5; DB 2; Length 361;

Best Local Similarity 67.3%; Pred. No. 4e-99;

Matches 230; Conservative 45; Mismatches 64; Indels 3; Gaps 2;

Qy 17 LTPQGGPHCLIPHLCLTFSLFGRSVNNFLITGPRAVLYTTTSVALGAQSGIECKFOF 76

Db 1 MNPQIFASLVMSI-CCHIIISSTAMSVNNFLITGPRAVLYTTTSVALGAQSGIECKFOF 59

Qy 77 AMERWNCPEVALQSTHNRISATRETSPIHAISSAGVWYITTKNSMGDFEN--CCDGG 134

Db 60 AMERWNCPEVALQSTHNRISATRETSPIHAISSAGVWYITTKNSMGDFENCCDGG 119

Qy 135 SNNGKTGHHIMWGCSNDVEFGERISKLFPVDSLEKGRDARALMNLHNNRAGRLAVRAATM 194

Db 120 SKTGKMGGRGHWVGGCSNDVNFGRILAKLPVDLHNGHSRAVNLHNEAGRLAVKATL 179

Qy 195 KRCKCKHIGSGSSSIQTCTWLAFFREMGDYLAQYDQALTIEMDKRQLRAGNSAEGHWV 254

Db 180 KRCKCKHIGSGSSSIQTCTWLAFFREMGDYLAQYDQALTIEMDKRQLRAGNSAEGHWV 239

Qy 255 PAENFLPSAEALIFLESPPDYCTGNSLGIYGTGEBRCLQNSHNTSRMRERSCGRLCTE 314

Db 240 IADTFSAVAGTELIIFMEDSPDYCTGNSLGIYGTGEBRCLQNSHNTSRMRERSCGRLCTN 299

Qy 315 CGLOVEERKTEVISSCNCKFQWCTVKCDQCRHVSXYKCAR 356

Db 300 ACTLVEERRLIETVSSCNCKFHMWCTVCKEQTCTGTTRKFCAR 341

RESULT 4

150506

gene wnt8b protein - zebra fish

C/Species: Brachydanio rerio (zebra fish)

C/Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 24-Nov-1999

C/Accession: 150506

R/Kelly, G.M.; Greenstein, P.; Erezylmaz, D.F.; Moon, R.T.

Development 121, 1787-1799, 1995

A/Title: Zebrafish wnt8 and wnt8b share a common activity but are involved in distinct

A/Reference number: 150506; MUID:95324404; PMID:7600994

A/Accession: 150506

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-358 <KEL>

A/Cross-references: EMBL:U10870; NID:9968916; PID:9968917

C/Genetics:

C/Supfamily: int-1 transforming protein

Query Match 59.7%; Score 1215.5; DB 2; Length 358;

Best Local Similarity 67.3%; Pred. No. 3.7e-93;

Matches 214; Conservative 42; Mismatches 57; Indels 5; Gaps 2;

Qy 40 GRSVNNFLITGPRAVLYTTTSVALGAQSGIECKFOFAMERNPCPNALQSTHNRISATR 99

Db 23 GRSVNNFLITGPRAVLYTTTSVALGAQSGIECKFOFAMERNPCPNALQSTHNRISATR 82

Qy 100 TRETSTHAISSAGVWYITTKNSMGDFENCGDSSNNKKTGGHIMWGCSNDVEFGER 159

Db 83 TRETSTHAISSAGVWYITTKNSMGDFENCGDSSNNKKTGGHIMWGCSNDVEFGER 142

Qy 160 ISLTFDSLEKGRDARALMNLHNNRAGRLAVRAATMRTCKKIGISSCSIQTCTWLAFFRE 219

Db 143 ISLTFDSLEKGRDARALMNLHNNRAGRLAVRAATMRTCKKIGISSCSIQTCTWLAFFRE 202

Qy 220 REMGDVLLAKKYDQALTIEMDKRQLR-AGNSAEGHWVPAEAFIPSAEALIFLESPPDYCT 278

Db 203 REMGDVLLAKKYDQALTIEMDKRQLR-AGNSAEGHWVPAEAFIPSAEALIFLESPPDYCT 258

Qy 279 CNSLGIYGTGEBRCLQNSHNTSRMRERSCGRLCTECGLQVEERKTEVISSCNCKFQWCC 338

Db 259 ENRTLGPTEGEBRCLQNSHNTSRMRERSCGRLCTECGLQVEERKTEVISSCNCKFQWCC 318

Qy 339 TVKCDQCRHVSXYKCAR 356

Db 319 AVKCEQCRKTVVYKVCAR 336

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OM protein - protein search, using SW model

Run on: January 30, 2004, 13:23:24 ; Search time 17 seconds

(without alignments)
1020.756 Million cell updates/sec

Title: US-09-898-456-7

Perfect score: 2037
Sequence: 1 MLCICQLCLVSPPTLTPC.....SKYYCARSPGSAQSLGKSA 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1791	87.9	355	WN8A_HUMAN	Q911J5 homo sapien
2	1496	73.4	354	WN8A_MOUSE	Q64527 mus musculu
3	1388	68.1	358	WN8B_XENLA	P28026 xenopus lae
4	1379	67.7	357	WN8C_CHICK	P51030 gallus gall
5	1316.5	64.6	359	WN8B_BRARE	P51028 brachydanio
6	1236	60.7	350	WN8B_MOUSE	Q64526 mus musculu
7	1215.5	59.7	358	WN8B_BRARE	P51029 brachydanio
8	1213	59.5	351	WN8B_HUMAN	Q91098 homo sapien
9	1155	56.7	428	WN8B_XENLA	P31291 xenopus lae
10	672.5	33.0	360	WN8C_XENLA	P31945 xenopus lae
11	657.5	32.3	351	WN8A_XENLA	P49138 xenopus lae
12	656.5	32.2	359	WN8A_AMBME	Q06442 ambystoma m
13	655.5	32.2	357	WN8B_AMBME	Q06443 ambystoma m
14	654.5	32.1	359	WN8A_PLEVA	O13267 pleurodeles
15	652.5	32.0	370	WN8B_BRARE	P24257 brachydanio
16	650.5	31.9	391	WN8B_HUMAN	Q91097 homo sapien
17	649.5	31.9	359	WN8B_HUMAN	Q91177 homo sapien
18	649.5	31.9	389	WN8B_MOUSE	O70283 mus musculu
19	648	31.8	351	WN8A_HUMAN	P56705 homo sapien
20	647.5	31.8	351	WN8B_XENLA	P81387 xenopus lae
21	646	31.7	351	WN8A_RAT	Q91095 rattus norv
22	644	31.6	351	WN8A_MOUSE	P22724 mus musculu
23	643.5	31.6	360	WN8A_MOUSE	P21552 mus musculu
24	643	31.6	350	WN8B_BRARE	Q91048 brachydanio
25	640.5	31.4	360	WN8B_HUMAN	P09544 homo sapien
26	640.5	31.4	380	WN8A_XENLA	P31286 xenopus lae
27	639	31.4	369	WN8B_AMBME	P21551 ambystoma m
28	638.5	31.3	359	WN8B_MOUSE	P22726 mus musculu
29	637	31.3	351	WN8A_CHICK	P49137 gallus gall
30	636.5	31.2	363	WN8B_BRARE	Q91050 brachydanio
31	636.5	31.2	365	WN8A_HUMAN	P41221 homo sapien
32	636	31.2	370	WN8B_HUMAN	P04628 homo sapien
33	636	31.2	370	WN8B_MOUSE	P04426 mus musculu

34	635	31.2	352	1	WN8A_XENLA	P31285 xenopus lae
35	634.5	31.1	371	1	WN8B_ORYLA	O42122 oryzae lat
36	632	31.0	353	1	WN8B_HALRO	O15978 halocynthia
37	629	30.9	352	1	WN8A_MOUSE	P27467 mus musculu
38	628	30.8	379	1	WN8A_RAT	Q91097 rattus norv
39	626	30.7	355	1	WN8B_HUMAN	P56703 homo sapien
40	626	30.7	355	1	WN8B_MOUSE	P17553 mus musculu
41	625	30.7	352	1	WN8A_HUMAN	P56704 homo sapien
42	623	30.6	379	1	WN8A_MOUSE	P22725 mus musculu
43	619.5	30.4	349	1	WN8B_MOUSE	P28047 mus musculu
44	617.5	30.3	349	1	WN8B_HUMAN	P56706 homo sapien
45	615.5	30.2	371	1	WN8A_XENLA	P10108 xenopus lae

ALIGNMENTS

RESULT 1
ID WN8A_HUMAN STANDARD; PRT; 355 AA.
AC Q911J5; Q96551;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Wnt-8a protein precursor (Wnt-8d).
GN WNT8A OR WNT8D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21301559; Pubmed=11408932;
RA Saitoh T., Katoh M.;
RT "Molecular cloning and characterization of human WNT8A.";
RL Int. J. Oncol. 19:123-127(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Teata T.T., Mosekowska D.E., Carter P.S., Hu E., Zhu Y.,
RA Kulshel D.P., Murodock P.R., Herrity N.C., Lewis C.J., Crose D.A.,
RA Culbert A.A., Reith A.D., Barnes M.R.;
RT "Molecular cloning and characterization of six novel human WNT
genes.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
TRANSMEMBRANE RECEPTORS. MAY PLAY AN IMPORTANT ROLE IN THE
DEVELOPMENT AND DIFFERENTIATION OF CERTAIN FOREBRAIN STRUCTURES,
NOTABLY THE HIPPOCAMPUS.
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
extracellular matrix.
CC -!- SIMILARITY: Belongs to the Wnt family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@ebi.ac.uk).
CC
CC EMBL; AB057725; BAB60960.1; -
CC EMBL; AY009402; AAG38662.1; -
CC Genew; HGNC:12788; WNT8A.
CC
CC MIM; 606360; -
CC InterPro; IPR005817; Wnt.
CC InterPro; IPR005816; Wnt_glycophorin.
CC Pfam; PF00110; wnt; 1.
CC PRINTS; PR01349; WNTPROTEIN.
CC SMART; SM00097; WNT1; 1.
CC PROSITE; PS00246; WNT1; 1.
CC Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.
CC SIGNAL 1 19 POTENTIAL.
CC CHAIN 20 355 WNT-8A PROTEIN.
CC FT

FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 348 355 RMEGVT -> KGSA (IN REF. 1).
 FT SEQUENCE 355 AA; 39527 MW; 605B1D5D755FBDB CRC64;
 Query Match 87.9%; Score 1791; DB 1; Length 355;
 Best Local Similarity 97.9%; Pred. No. 2,1e-147;
 Matches 327; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 33 CLTSLGRSVNNLTGPKAYLTFTTSVALGAQSGIECKFOFAMERNCPENALQST 92
 DB 15 CAASFASASVNNLTGPKAYLTFTTSVALGAQSGIECKFOFAMERNCPENALQST 74
 QY 93 HNRLSATRETSFTHAISSAGVMTITNCGMDPENCGCGSNNGKTGHWIMGCGSD 152
 DB 75 HNRLSATRETSFTHAISSAGVMTITNCGMDPENCGCGSNNGKTGHWIMGCGSD 134
 QY 153 NVEGERISKLVDSLEKGDARALMNLHNNRAGRLAVRATMKRTCKCHGISGCSIQTC 212
 DB 135 NVEGERISKLVDSLEKGDARALMNLHNNRAGRLAVRATMKRTCKCHGISGCSIQTC 194
 QY 213 WLQLAEPREMGDIYKAKYDQALKTMDKROLRAGNSAGHWVPAEALPLPSAEALIFLEE 272
 DB 195 WLQLAEPREMGDIYKAKYDQALKTMDKROLRAGNSAGHWVPAEALPLPSAEALIFLEE 254
 QY 273 SPDYCTCNSSLGITGREGCLONSHNTSRMERSCGRLCTEGCLOVERKTEVSISSCNC 332
 DB 255 SPDYCTCNSSLGITGREGCLONSHNTSRMERSCGRLCTEGCLOVERKTEVSISSCNC 314
 QY 333 KFWMCCTVCKDQCRHVSKYKCARSPGSAQSLGR 366
 DB 315 KFWMCCTVCKDQCRHVSKYKCARSPGSAQSLGR 348

RESULT 2
 WN8A_MOUSE STANDARD; PRT; 354 AA.
 ID WN8A_MOUSE
 AC 064527;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Wnt-8a protein precursor (Wnt-8d) (Stimulated by retinoic acid protein 11) (Wnt-8).
 DE 11) (Wnt-8).
 GN WNT8A OR WNT8D OR STRA11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=97042052; PubMed=8887323;
 RA Bouillet P.; Oulad-Abdelghani M.; Ward S.J.; Bronner S.; Chambon P.;
 RA Doile P.;
 RT "A new mouse member of the Wnt gene family, wnt-8, is expressed during early embryogenesis and is ectopically induced by retinoic acid".
 RT Mech. Dev. 58:141-152(1996).
 RL -1- FUNCTION: Ligand for members of the frizzled family of seven transmembrane receptors. Probable developmental protein. May be a signaling molecule which affects the development of discrete regions of tissues. Is likely to signal over only few cell diameters (By similarity).
 CC -1- SUBCELLULAR LOCATION: Possibly secreted and associates with the extracellular matrix.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION IN EARLY STAGES OF EMBRYOGENESIS. EXPRESSION BEGINS IN THE POSTERIOR REGION OF EARLY PRIMITIVE STREAK-STAGE EMBRYOS AND AFTER IT SPREADS INTO THE EMBRYONIC ECTODERM UP TO A SHARP ROSTRAL BOUNDARY AT THE BASE OF THE DEVELOPING HEADFOLDS. EXPRESSED TRANSIENTLY IN THE NEWLY FORMED MESODERM. EXPRESSION IS DOWN-REGULATED DURING SOMITOGENESIS. THE EXPRESSION IS HIGHLY RESTRICTED DURING GASTRULATION AND

CC NEURULATION, BOTH TEMPORALLY AND SPATIALLY.
 CC -1- INDUCTION: By retinoic acid.
 CC -1- SIMILARITY: Belongs to the Wnt family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Z68889; CA93117.1; --
 CC MGD; MGI:107924; Wnt8a.
 CC InterPro; IPR005817; Wnt.
 CC InterPro; IPR005816; Wnt_glyfactor.
 CC Pfam; PF00110; wnt; 1.
 CC PRINTS; PR01349; WNTPROTEIN.
 CC SMART; SM00097; WNT1; 1.
 CC PROSITE; PS00246; WNT1; 1.
 CC Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.
 CC SIGNAL 1 19
 FT CHAIN 20 354 WNT-8A PROTEIN.
 FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 354 AA; 39473 MW; 1CA5E83840184D9 CRC64;
 Query Match 73.4%; Score 1496; DB 1; Length 354;
 Best Local Similarity 82.5%; Pred. No. 6,4e-122;
 Matches 269; Conservative 22; Mismatches 35; Indels 0; Gaps 0;

QY 42 SVNNFLTGPKAYLTFTTSVALGAQSGIECKFOFAMERNCPENALQSTHRLSATR 101
 DB 24 SVNNFLTGPKAYLTFTTSVALGAQSGIECKFOFAMERNCPENALQSTHRLSATR 83
 QY 102 ETSFTHAIRSAALIMVATYKNSGMDLENCGDSSQNKKTGHWIMGCGSDNVEFGKIS 161
 DB 84 ETSFTHAIRSAALIMVATYKNSGMDLENCGDSSQNKKTGHWIMGCGSDNVEFGKIS 143
 QY 162 KLFVDSLEKGDARALMNLHNNRAGRLAVRATMKRTCKCHGISGCSIQTCWLQLAEPRE 221
 DB 144 KLFVDSLEKGDARALMNLHNNRAGRLAVRATMKRTCKCHGISGCSIQTCWLQLAEPRE 203
 QY 222 MGDYLAKEYDQALKTMDKROLRAGNSAGHWVPAEALPLPSAEALIFLESPDYCTCNS 281
 DB 204 MGDYLAKEYDQALKTMDKROLRAGNSAGHWVPAEALPLPSAEALIFLESPDYCTCNS 263
 QY 282 SLGTYGREGCLONSHNTSRMERSCGRLCTEGCLOVERKTEVSISSCNCCKPOMCCTVK 341
 DB 264 SLGTYGREGCLONSHNTSRMERSCGRLCTEGCLOVERKTEVSISSCNCCKPOMCCTVK 323
 QY 342 CDGCRHVSKYKCARSPGSAQSLGK 367
 DB 324 CDGCRHVSKYKCARSPGSAQSLGK 349

RESULT 3
 WN8A_XENLA STANDARD; PRT; 358 AA.
 ID WN8A_XENLA
 AC P28026;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Wnt-8 protein precursor (XWnt-8).
 GN WNT-8.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91347916; PubMed=1879349;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 30, 2004, 13:26:30 ; Search time 41 Seconds
(without alignments)
2322.473 Million cell updates/sec

Title: US-09-898-456-7

Perfect score: 2037
Sequence: 1 MLCCTCQLCLVSPPTLTPC.....SKYYCARSPGASGLGKSA 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_todent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archaeosp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	1415	69.5	381	13	Q90Z23 ambystoma m
2	1266	62.2	354	13	Q90Y18 brachydania
3	1266	62.2	354	13	Q90Y18 brachydania
4	1243	61.0	368	11	Q8BQD1 mus musculus
5	994.5	48.8	364	5	Q9U416 mus musculus
6	978	48.0	364	5	Q9U416 mus musculus
7	676.5	33.2	315	13	Q9PUI3 gallus galli
8	676.5	33.2	385	13	Q988N7 gallus galli
9	661.5	32.5	387	13	Q8AY89 brachydania
10	656	32.2	351	11	Q8IUM6 mus musculus
11	650.5	31.9	311	11	Q9CZK3 mus musculus
12	647.5	31.8	360	11	Q9CZK3 mus musculus
13	647.5	31.8	360	11	Q9CZK3 mus musculus
14	638.5	31.3	372	11	Q91XF5 mus musculus
15	638.5	31.3	374	5	Q8T396 cupiemus
16	637.5	31.3	374	5	Q8T396 cupiemus

17	636.5	31.2	360	11	Q8BM17 mus musculus
18	636.5	31.2	360	11	Q8BVC6 mus musculus
19	635.5	31.2	370	5	P79752 fugu rubrip
20	633	31.1	370	5	Q8W575 brachydania
21	633	31.1	376	13	Q9PMH1 gallus galli
22	632.5	31.1	353	5	Q9T2T6 mus musculus
23	632.5	31.1	371	5	Q8T8A8 halocynthia
24	632.5	31.1	380	11	Q8BMP9 mus musculus
25	629.5	30.9	385	13	Q9YXG6 gallus galli
26	626	30.7	329	11	Q8BLT2 mus musculus
27	619.5	30.4	349	13	Q42258 xenopus lae
28	618	30.3	360	5	Q9U6V0 ciona intes
29	617	30.3	350	13	Q8UR39 fugu rubrip
30	617	30.3	377	5	Q61699 brachydania
31	611.5	30.0	394	5	Q9GRA6 gryllus bim
32	610.5	30.0	347	5	Q61700 brachydania
33	609.5	29.9	364	11	Q8C6P4 mus musculus
34	608.5	29.9	352	5	Q9V584 drosophila
35	607.5	29.8	270	5	Q8MPJ3 platyneris
36	606.5	29.8	375	5	Q8MPJ6 platyneris
37	602.5	29.6	349	13	Q9DEB8 gallus galli
38	601	29.5	358	13	Q91AU3 brachydania
39	600.5	29.5	349	4	Q96H90 homo sapien
40	600.5	29.5	349	11	Q9DBY3 mus musculus
41	599.5	29.4	363	5	Q9GTU9 hydra atten
42	597	29.3	358	5	Q8MPJ8 platyneris
43	594.5	29.2	331	5	Q96867 stronglyloce
44	593	29.1	415	5	Q8P111 drosophila
45	589	28.9	365	4	Q8N2E5 homo sapien

ALIGNMENTS

RESULT 1

ID Q90Z23 PRELIMINARY; PRT; 381 AA.

AC Q90Z23; 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Secreted Factor Axwnt-8.

GN Wnt-8.

OS Ambystoma mexicanum (Axolotl).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomataceae;

OC Ambystoma.

OX NCBI TaxID=8296;

RN (1)

RP SEQUENCE FROM N.A.

RA Bachvarova R.P., Masi T., Thomas J., Hall L., Johnson A.D.;

RT "Formation of posterior ventrolateral mesoderm in the urodele,

RL Ambystoma mexicanum: expression of Axwnt-8.";

CC Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE

CC EXTRACELLULAR MATRIX (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.

CC EMBL, AF308871; AKS8845.1; -.

DR InterPro; IPR005817; Wnt.

DR Pfam; PF00110; wnt.1.

DR PRINTS; PR01349; WNTPROTEIN.

DR SMART; SM00097; WNT1.1.

DR PROSITE; PS00246; WNT1.1.

KW Developmental protein; Glycoprotein.

SEQUENCE 381 AA; 42728 MW; 6A392F9C15FA64F4 CRC64;

Query Match 69.5%; Score 1415; DB 13; Length 381;

Best Local Similarity 75.9%; Pred. No. 3.8e-130;

Matches 246; Conservative 41; Mismatches 37; Indels 0; Gaps 0;

QY 33 CLTFLSGRSVNNFLITGPAYLYLTTSVALGAQSGIECKFOFAMERNKCPENALQLST 92


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Db      16  CTITASASVNNLMTGPKAYLTYSTSVAGASGIECKFOFAMERNWCPESALOST 75
Qy      93  HNRFSATRETSFTHATISSAGWYITKNCMGDPENCDCGSGNNKGTGHWIWGCGSD 152
Db      76  HNGRSATRETSFTHATISSAGWYITKNCMGDPENCDCGSGNNKGTGHWIWGCGSD 135
Qy      153 NVEFGERISKLFDVLSLEKGDARALMLNHNRAGLAVRATMKRTCKHGSGSISQTC 212
Db      136 NVDFGERISKEFVDALETGDSRALMHNNEAGFAVKSIMKRTCKHGSGSISQTC 195
Qy      213 WLQLAEREMDDYKAKYDQKLEMDKQRLRAGNSAGHWVPAPFLPSAEALIFEE 272
Db      196 WLQLAEREDIGNYKIKHDKALKLEMDKRRRAGNSADNRGAIEAFSLVATELIFED 255
Qy      273 SPDYCTGSSSLGIGTEGREGCLONSHNTRMWRSSCGRLCTEGLOVERKTEIVSSCNC 332
Db      256 SPDYCLRNASLGLDQTEGREGCLONSHNTRMWRSSCGRLCTEGLOVERKTEIVSSCNC 315
Qy      333 KFWCCCTVCKDCRHWVSKYYCAR 356
Db      316 KFWCCCTVCKDCRHWVSKYYCAR 339

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RESULT 2

```

ID 090YL8 PRELIMINARY; PRT; 354 AA.
AC 090YL8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Wnt8-like protein 2.
GN Wnt8.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Lekven A.C., Thorpe C.J., Waxman J.S., Moon R.T.;
RT "Zebrafish wnt8 encodes two wnt8 proteins on a bicistronic transcript
RT and is required for mesoderm and neurotoderam patterning.";
RL Dev. Cell 1:0-0(2001).
DR EMBL: AY032749; AAK70224.1; -
DR InterPro: IPR005817; Wnt_
DR InterPro: IPR005816; Wnt_grtfactor.
DR Pfam: PF00110; wnt, 1.
DR PRINTS: PRO1349; WNTPROTEIN.
DR SMART: SM00097; WNT1, 1.
SQ SEQUENCE 354 AA; 40109 MW; F42951A27AC38A67 CRC64;

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Query Match      62.2%; Score 1266; DB 13; Length 354;
Best Local Similarity 69.0%; Pred. No. 1,4e-115;
Matches 220; Conservative 44; Mismatches 55; Indels 0; Gaps 0;

Qy 42 SVNNFLITGPKAYLYTTTSVALGASGIECKFOFAMERNWCPENALQSTHNRLSRATR 101
Db 24 TNNMLITGPKAYLYTTTSVALGASGIECKFOFAMERNWCPENALQSTHNRLSRATR 83
Qy 102 ETSFTHATISSAGWYITKNCMGDPENCDCGSGNNKGTGHWIWGCGSDNVEFGERIS 161
Db 84 ESSFVHAISAAGWYITLIRNCSLDLNECGDSSRNGLRGWLMGCGSDNVEFGERIS 143
Qy 162 KLFVDSLEKGDARALMLNHNRAGLAVRATMKRTCKHGSGSISQTCWLQLAERFRE 221
Db 144 KQFVDALETGQDARAANVLAHNEAGRLAVKATMKRIRCRHGMSBSCTMOTCMQDLADFRE 203
Qy 222 MGDYTKAKYDQALKLEMDKQRLRAGNSAGHWVPAPFLPSAEALIFLESPPDYCTGNS 281
Db 204 IGNLYKVKHDOQKLEMDKRRRAGNSADNRVYMTTDAFSGIARTELLYLSDSPDYCKNL 263
Qy 282 SLGIYGTGREGCLONSHNTRMWRSSCGRLCTEGLOVERKTEIVSSCNCCKFOMCCTVK 341

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Db      264 SLGIYGTGREGCLONSHNTRMWRSSCGRLCTEGLOVERKTEIVSSCNCCKFOMCCTVK 323
Qy      342 CDGCRHWVSKYYCARSPGS 360
Db      324 CENCSQYTVHGVCTRRHGS 342

```

RESULT 3

```

ID 090YJ8 PRELIMINARY; PRT; 354 AA.
AC 090YJ8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Wnt8-like protein 2.
GN Wnt8.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Lekven A.C., Thorpe C.J., Waxman J.S., Moon R.T.;
RT "Zebrafish wnt8 encodes two wnt8 proteins on a bicistronic transcript
RT and is required for mesoderm and neurotoderam patterning.";
RL Dev. Cell 1:0-0(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Lekven A.C., Thorpe C.J., Waxman J.S., Moon R.T.;
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: U10869; AAK68628.1; -
DR ZFIN: ZDB-GENE-980526-332; wnt8.
DR InterPro: IPR005817; Wnt_
DR InterPro: IPR005816; Wnt_grtfactor.
DR Pfam: PF00110; wnt, 1.
DR PRINTS: PRO1349; WNTPROTEIN.
DR SMART: SM00097; WNT1, 1.
SQ SEQUENCE 354 AA; 40065 MW; B25CEDF87453FD37 CRC64;

```

```

Query Match      62.2%; Score 1266; DB 13; Length 354;
Best Local Similarity 69.0%; Pred. No. 1,4e-115;
Matches 220; Conservative 44; Mismatches 55; Indels 0; Gaps 0;

Qy 42 SVNNFLITGPKAYLYTTTSVALGASGIECKFOFAMERNWCPENALQSTHNRLSRATR 101
Db 24 TNNMLITGPKAYLYTTTSVALGASGIECKFOFAMERNWCPENALQSTHNRLSRATR 83
Qy 102 ETSFTHATISSAGWYITKNCMGDPENCDCGSGNNKGTGHWIWGCGSDNVEFGERIS 161
Db 84 ESSFVHAISAAGWYITLIRNCSLDLNECGDSSRNGLRGWLMGCGSDNVEFGERIS 143
Qy 162 KLFVDSLEKGDARALMLNHNRAGLAVRATMKRTCKHGSGSISQTCWLQLAERFRE 221
Db 144 KQFVDALETGQDARAANVLAHNEAGRLAVKATMKRIRCRHGMSBSCTMOTCMQDLADFRE 203
Qy 222 MGDYTKAKYDQALKLEMDKQRLRAGNSAGHWVPAPFLPSAEALIFLESPPDYCTGNS 281
Db 204 IGNLYKVKHDOQKLEMDKRRRAGNSADNRVYMTTDAFSGIARTELLYLSDSPDYCKNL 263
Qy 282 SLGIYGTGREGCLONSHNTRMWRSSCGRLCTEGLOVERKTEIVSSCNCCKFOMCCTVK 341
Db 264 SLGIYGTGREGCLONSHNTRMWRSSCGRLCTEGLOVERKTEIVSSCNCCKFOMCCTVK 323
Qy 342 CDGCRHWVSKYYCARSPGS 360
Db 324 CENCSQYTVHGVCTRRHGS 342

RESULT 4
Q8BOD1 PRELIMINARY; PRT; 368 AA.
ID 08BOD1

```

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 30, 2004, 13:27:50 ; Search time 21 Seconds
(without alignments)
743.462 Million cell updates/sec

Title: US-09-898-456-7

Perfect score: 2037
Sequence: 1 MLCICICLCVSPFPTLTPC.....SKYYCARSPGASLGKSA 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	640.5	31.4	360	US-09-417-039-4	Sequence 4, Appl
2	636.5	31.2	365	US-09-417-039-9	Sequence 9, Appl
3	636	31.2	351	US-09-067-782A-2	Sequence 2, Appl
4	636	31.2	370	US-09-417-039-3	Sequence 3, Appl
5	634.5	31.1	359	US-09-082-089-3	Sequence 3, Appl
6	634.5	31.1	363	US-09-082-089-5	Sequence 5, Appl
7	634.5	31.1	372	US-09-082-089-2	Sequence 2, Appl
8	626	30.7	355	US-09-082-270-2	Sequence 2, Appl
9	620.5	30.5	397	US-08-647-928-8	Sequence 8, Appl
10	600.5	29.5	349	US-09-459-774-2	Sequence 2, Appl
11	600.5	29.5	349	US-09-903-817-2	Sequence 2, Appl
12	593.5	29.1	349	US-09-417-039-7	Sequence 7, Appl
13	593.5	29.1	389	US-08-485-449-2	Sequence 2, Appl
14	593.5	29.1	389	US-08-485-449-7	Sequence 7, Appl
15	528.5	25.9	389	US-08-485-449-6	Sequence 6, Appl
16	487	23.9	376	US-08-485-449-5	Sequence 5, Appl
17	370.5	18.2	159	US-09-082-270-4	Sequence 4, Appl
18	268	13.2	133	US-09-417-039-5	Sequence 5, Appl
19	222	10.9	121	US-09-067-782A-5	Sequence 5, Appl
20	216	10.6	120	US-09-417-039-6	Sequence 6, Appl
21	209	10.3	124	US-09-417-039-8	Sequence 8, Appl
22	155	7.6	131	US-09-067-782A-4	Sequence 4, Appl
23	104	5.1	788	US-08-918-914-4	Sequence 4, Appl
24	101	5.0	1193	US-08-400-159-10	Sequence 10, Appl
25	101	5.0	1193	US-08-611-729A-10	Sequence 10, Appl
26	99.5	4.9	642	US-08-872-855-10	Sequence 10, Appl
27	97	4.8	24	US-08-726-867A-10	Sequence 10, Appl

28	97	4.8	24	3	US-08-942-806A-10	Sequence 10, Appl
29	96.5	4.7	1184	2	US-08-918-914-1	Sequence 1, Appl
30	96.5	4.7	1184	3	US-08-996-083-3	Sequence 3, Appl
31	95	4.7	488	1	US-08-243-542-1	Sequence 1, Appl
32	95	4.7	488	1	US-08-477-407-1	Sequence 1, Appl
33	95	4.7	488	1	US-08-484-355-1	Sequence 1, Appl
34	95	4.7	524	1	US-08-243-542-2	Sequence 2, Appl
35	95	4.7	524	1	US-08-477-407-2	Sequence 2, Appl
36	95	4.7	524	1	US-08-484-355-2	Sequence 2, Appl
37	95	4.7	670	1	US-08-453-542-3	Sequence 3, Appl
38	95	4.7	670	1	US-08-477-407-3	Sequence 3, Appl
39	95	4.7	670	1	US-08-484-355-3	Sequence 3, Appl
40	95	4.7	769	1	US-08-243-542-4	Sequence 4, Appl
41	95	4.7	769	1	US-08-477-407-4	Sequence 4, Appl
42	95	4.7	769	1	US-08-484-355-4	Sequence 4, Appl
43	95	4.7	1016	3	US-08-882-046-7	Sequence 7, Appl
44	95	4.7	1036	4	US-09-068-740A-6	Sequence 6, Appl
45	95	4.7	1187	4	US-09-068-740A-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-417-039-4
Sequence 4, Application US/09417039A
Patent No. 6485972
GENERAL INFORMATION:
APPLICANT: McMahon, Andrew P.
APPLICANT: Parr, Brian A.
TITLE OF INVENTION: WNT SIGNALING IN REPRODUCTIVE ORGANS
FILE REFERENCE: 00246/232001
CURRENT APPLICATION NUMBER: US/09/417, 039A
CURRENT FILING DATE: 1999-10-12
EARLIER APPLICATION NUMBER: US 60/109,355
EARLIER FILING DATE: 1998-10-15
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-09-417-039-4

Query Match 31.4%; Score 640.5; DB 4; Length 360;

Best Local Similarity 40.8%; Pred. No. 5.1e-58;
Matches 125; Conservative 54; Mismatches 108; Indels 19; Gaps 7;

QY	60	SVALGAOSGIECKFOFAMERNANCENALQLSYHNR-LRSATRETSFIHAISSAGWYII	118
DB	64	AIOGVAEMTAECOHQROHRCNLTDRHSLFGRVLRRSSRESAFVAISSAGVFAI	123
QY	119	TKNCSMGDFENCCDGSNNKGTGHWI--WGCSDNVEFERISIKLFVDSL-KGDKAR	175
DB	124	TRACSGCEVSCSCDPEKMSADSKGIFPMWGCSDIDYIGIFARAFVDAKERKGDAR	183
QY	176	ALMNLHNRGRGLAVATMKTCKGICSGSSCIOTCMQLAFREMGDVLKAYDQAK	235
DB	184	ALMNLHNRGRGRAVVKFLKQCKCHGVSGCTLRICWLMADPRKTGDLMKRYNAIQ	243
QY	236	IEMDKQLRAGNSAEGHVPAEAFILPSABEALFLFLESPDYCTNSLIGYEGRECLQ	295
DB	244	VVWNO-----DGTGTVANERFKPTKNDIVFENSPPYCIKDRRAGSLGTAGRCNL	296
QY	296	NSNHTSRERRSGRLCTECGLQVERKTEVISCNCKCFQWCTVKCDQCRHVVSKYYCA	355
DB	297	TSRGM-----SCEVNC--CGRGYDTSHTVMTKCKGCFMCAVCCODLEALDVHTC-	348
QY	356	RSPGSA 361	
DB	349	KAPKNA 354	

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RESULT 2
US-09-417-039-9
; Sequence 9, Application US/09417039A
; Patent No. 6485972
; GENERAL INFORMATION:
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Parr, Brian A.
; APPLICANT: Vaino, Seppo
; TITLE OF INVENTION: WNT SIGNALLING IN REPRODUCTIVE ORGANS
; FILE REFERENCE: 00246/232001
; CURRENT APPLICATION NUMBER: US/09/417.039A
; CURRENT FILING DATE: 1999-10-12
; EARLIER APPLICATION NUMBER: US 60/109,355
; EARLIER FILING DATE: 1998-10-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-417-039-9

Query Match          31.2%; Score 636.5; DB 4; Length 365;
Best Local Similarity 40.2%; Pred. No. 1.4e-57;
Matches 125; Conservative 52; Mismatches 107; Indels 27; Gaps 8;

QY 54 YLTITTSVALAAGSGIEBCKQFAMERNCPENALQSTHNR-LSATRETSFTHAISSA 112
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 71 YQDMQYIGEGAKGKIGECQYQFRRHWNQ-STVDNITSVFGRVMOISRETAFTYAVSAA 129
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 113 GWMIITRNKCMGDFENCGCDGSNNKGTGHWIMGCGSDNVEFGERISKLFVDSLE--- 169
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 130 GVVNAMSRAKREGSLSTGCGRRARPDLPRDMLMGCGDNIDGYFAKGFVARERER 189
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 170 ---KG--KDAALNMLHNRAAGRLAVRATMRKCKCHGISGCSIQTCTWLQLAEFREMGD 224
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 190 IHAGSYESARILNMLHNNEAGRTVYVLADVACKCHGVSGCSLKTCLQLADFRKVD 249
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 225 YLRKAKYQALKIEMDKR-QLPAGNSAEGHWPAEAFPSAEALIFLEESPDYCTCSSL 283
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 250 ALKERYSAAMRLNNSRGKLVQVNS-----RFSNPTTQDLVYIDPSPDYCVRNEST 300
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 284 GIVTEGREGCLONSHNTRSMWRERSCGRLCTECGLOVEERKTEVISGNCCKFQWCCYKCD 343
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 GSLGTGRLCKTKTEGMD-----GCELMC--CGRGYDQFKTVQIERCHCKHMCYVCKK 353
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 344 QCRHVNSKYYC 354
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 354 KCTEIVDQFVC 364
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RESULT 3
US-09-067-782A-2
; Sequence 2, Application US/09067782A
; Patent No. 6165751
; GENERAL INFORMATION:
; APPLICANT: BARNES, MICHAEL
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: US
; ZIP: 19482-0980
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/067,782A
FILING DATE: 28-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 9710734.6
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: EP 97309144.0
FILING DATE: 13-NOV-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-30167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 601-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-067-782A-2

Query Match          31.2%; Score 636; DB 3; Length 351;
Best Local Similarity 37.9%; Pred. No. 1.4e-57;
Matches 139; Conservative 49; Mismatches 119; Indels 60; Gaps 11;

QY 26 CLIPHLCLTFLSPGRSNVFLITGP-----KAYLTYT 58
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 CLRSRL-LVFAVFAASAASNMLYAKLSVGSISEETCEKGLIORQVOMCRNLEVM 64
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 59 TSVALGAGOSIEBCKQFAMERNCPENALQSTHNR-----NSATRETSFTHAISS 111
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 DSVARGQLAIECQYQFRRHWNQ-----STLDSLPGVGYVTQIGIEALVVAISS 117
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 112 AGWMIITRNKCMGDFENCGCDGSNNKGTGHWIMGCGSDNVEFGERISKLFVDSLEKG 171
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 118 AGVAFATVTRACSGSELEKCGCDRTVHG-VSPQGFQSGGSDNLAAGVAFQSTVDVRERS 176
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 172 KDA---RALNMLHNRAAGRLAVRATMRKCKCHGISGCSIQTCTWLQLAEFREMGDYKA 228
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 177 KGASSRSLNMLHNNEAGRTVYVLADVACKCHGVSGCSLKTCLQWRAVPFRQVGHALKE 236
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 229 KYQDALKIEMDKRQLPAGNSAEGHWPAEAFPSAEALIFLEESPDYCTCSSIGIYG 287
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 237 KFDGATEVE---PRVGSRA--LVPRNQQFPHTEDELVYLEPSPDFCEQDRSGVLG 290
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 288 TEGREGCLONSHNTRSMWRERSCGRLCTECGLOVEERKTEVISGNCCKFQWCCYKCDQCRH 347
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 291 TRGRTCKTKSKAID-----GCELLC--CGRGHTAQLVLAERSCKRFHMCFFVKCRQCR 343
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 348 VNSKYYC 354
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 344 LVELHTC 350
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RESULT 4
US-09-417-039-3
; Sequence 3, Application US/09417039A
; Patent No. 6485972
; GENERAL INFORMATION:
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Parr, Brian A.
; APPLICANT: Vaino, Seppo
; TITLE OF INVENTION: WNT SIGNALLING IN REPRODUCTIVE ORGANS
; FILE REFERENCE: 00246/232001
; CURRENT APPLICATION NUMBER: US/09/417.039A
; CURRENT FILING DATE: 1999-10-12
; EARLIER APPLICATION NUMBER: US 60/109,355
; EARLIER FILING DATE: 1998-10-15
; NUMBER OF SEQ ID NOS: 11
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OM protein - protein search, using SW model

Run on: January 30, 2004, 13:30:11 ; Search time 40 Seconds
(without alignments)
1917.177 Million cell updates/sec

Title: US-09-898-456-7
Perfect score: 2037
Sequence: 1 MLCICQCLVSPFPTLTPC.....SKYYCARPSASQSLGKSA 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 789580 seqs, 207824079 residues

Total number of hits satisfying chosen parameters: 789580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Published Applications_AA:*

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3: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*

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13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1808	88.8	351	12	US-10-275-115-2
2	1802	88.5	351	11	US-09-842-758-8
3	1791	87.9	355	11	US-09-842-758-44
4	1791	87.9	355	12	US-10-285-976-23
5	1783	87.5	355	14	US-10-005-947-2
6	1496	73.4	354	11	US-09-842-758-45
7	1496	73.4	354	14	US-10-005-947-4
8	1388	68.1	357	11	US-09-842-758-46
9	1379	67.7	357	12	US-09-842-758-47
10	1213	59.5	351	12	US-10-285-976-25
11	1137.5	47.8	295	14	US-10-005-947-6
12	973	47.8	176	12	US-10-029-386-32775
13	712	35.0	352	12	US-10-028-248A-71
14	649.5	31.9	359	12	US-10-285-976-15
15	649.5	31.9	359	12	US-10-295-027-584

16	648	31.8	351	10	US-09-978-295A-226	Sequence 226, App
17	648	31.8	351	10	US-09-978-697-226	Sequence 226, App
18	648	31.8	351	10	US-09-978-193A-226	Sequence 226, App
19	648	31.8	351	10	US-09-978-832A-226	Sequence 226, App
20	648	31.8	351	11	US-09-978-189-226	Sequence 226, App
21	648	31.8	351	11	US-09-978-608A-226	Sequence 226, App
22	648	31.8	351	11	US-09-978-585A-226	Sequence 226, App
23	648	31.8	351	11	US-09-978-191A-226	Sequence 226, App
24	648	31.8	351	11	US-09-978-403A-226	Sequence 226, App
25	648	31.8	351	11	US-09-978-564A-226	Sequence 226, App
26	648	31.8	351	11	US-09-999-833A-226	Sequence 226, App
27	648	31.8	351	11	US-09-981-915A-226	Sequence 226, App
28	648	31.8	351	11	US-09-978-82A-226	Sequence 226, App
29	648	31.8	351	11	US-09-918-585A-226	Sequence 226, App
30	648	31.8	351	11	US-09-978-423A-226	Sequence 226, App
31	648	31.8	351	11	US-09-978-193A-226	Sequence 226, App
32	648	31.8	351	11	US-09-978-830A-226	Sequence 226, App
33	648	31.8	351	11	US-09-978-757A-226	Sequence 226, App
34	648	31.8	351	11	US-09-978-187B-226	Sequence 226, App
35	648	31.8	351	11	US-09-978-643A-226	Sequence 226, App
36	648	31.8	351	12	US-09-978-375A-226	Sequence 226, App
37	648	31.8	351	12	US-09-978-188A-226	Sequence 226, App
38	648	31.8	351	12	US-09-978-298A-226	Sequence 226, App
39	648	31.8	351	12	US-10-143-031A-226	Sequence 226, App
40	648	31.8	351	12	US-10-002-967A-226	Sequence 226, App
41	648	31.8	351	12	US-10-017-083A-226	Sequence 226, App
42	648	31.8	351	12	US-10-143-030A-226	Sequence 226, App
43	648	31.8	351	12	US-10-199-672-80	Sequence 80, App1
44	648	31.8	351	12	US-10-187-749-80	Sequence 80, App1
45	648	31.8	351	12	US-10-194-457-80	Sequence 80, App1

ALIGNMENTS

RESULT 1
US-10-275-115-2
; Sequence 2, Application US/10275115
; Publication No. US20030175805A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: New winglees gene Wnt-8D
; FILE REFERENCE: WNT84KDS
; CURRENT APPLICATION NUMBER: US/10/275,115
; CURRENT FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-275-115-2

Query Match 88.8%; Score 1808; DB 12; Length 351;
Best Local Similarity 98.2%; Pred. No. 1.2e-168;
Matches 331; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	33	CLTFSLFGKRVNPLITGPAYITTTTSVALGAGSGIECKFPQPMWRNMCPEALDLS	92
DB	15	CAAFSASAMVNNFLITGPAYITTTTSVALGAGSGIECKFPQPMWRNMCPEALDLS	74
QY	93	HNRLRSATRETSFTHAISSAGVWYITTKNSMDFENCGDGSNGKTGGHWTGGCSD	152
DB	75	HNRLRSATRETSFTHAISSAGVWYITTKNSMDFENCGDGSNGKTGGHWTGGCSD	134
QY	153	NVEFGERISKLFVDSLEKGDARALNNLNHNRAGRLAVRAITMKRTCKHGISGCSIoTC	212
DB	135	NVEFGERISKLFVDSLEKGDARALNNLNHNRAGRLAVRAITMKRTCKHGISGCSIoTC	194
QY	213	WLOLAERREKVDILKAKYDALKIEMDKRLRAGNSHEGHWVAEFLPBAEMLTLEE	272
DB	195	WLOLAERREKVDILKAKYDALKIEMDKRLRAGNSHEGHWVAEFLPBAEMLTLEE	254

QY 273 SPDYCTCNSSIGIYGTGREGCLONSHNTSRWERRSCGRLCTEGLOVEERKTEVISSCNC 332
DB 255 SPDYCTCNSSIGIYGTGREGCLONSHNTSRWERRSCGRLCTEGLOVEERKTEVISSCNC 314
QY 333 KFWCCTVCKDQCGRHVSKYYCARSPGSAQSLGKGS 369
DB 315 KFWCCTVCKDQCGRHVSKYYCARSPGSAQSLGKGS 351

RESULT 2

US-09-842-758-8
Sequence 8, Application US/09842758
Publication No. US20030083244A1
GENERAL INFORMATION:
APPLICANT: Vernet, Corine A. M.
APPLICANT: Fernandes, Elma R.
APPLICANT: Gerlach, Valerie
APPLICANT: Shimkets, Richard A.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Zernhusen, Bryan D.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Majumder, Kumud
APPLICANT: Tcheneru, Velizar T.
APPLICANT: Padigaru, Muralidhara
APPLICANT: Burgess, Catherine E.
APPLICANT: Gangolli, Esha A.
APPLICANT: Smithson, Glenda
APPLICANT: Rastelli, Luca
APPLICANT: MacDougall, John R.
APPLICANT: Taupier, Raymond J.
APPLICANT: Grose, William M.
APPLICANT: Edward, Szekeres S.
APPLICANT: Alsobrook II, John P.
TITLE OF INVENTION: No. US20030083244A1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-783
CURRENT APPLICATION NUMBER: US/09/842,758
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/200,158
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 60/200,613
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,780
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/201,006
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,007
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,236
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,238
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,186
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/201,474
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/201,508
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/220,591
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/232,678
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/263,217
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/265,160
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 351
TYPE: PRT
ORGANISM: Homo sapiens

US-09-842-758-8

Query Match 88.5%; Score 1802; DB 11; Length 351;
Best Local Similarity 97.9%; Pred. No. 4,7e-168;
Matches 330; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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DB 15 CAAFSASAMSVNNFLITGPAYLITTTVALGASQSIGIECKFPFANERNKCPENALQLST 74
QY 93 HNRIRSATRETFSTFIHIISSAGVWYIITKNCMDGFENCGCGDGNNGTGHWIMGCS 152
DB 75 HNRIRSATRETFSTFIHIISSAGVWYIITKNCMDGFENCGCGDGNNGTGHWIMGCS 134
QY 153 NVEFGERISKLFDVDSLEKGDARALMNLHNNRAGRLAVRATMRCKCHGISGCSIQTC 212
DB 135 NVEFGERISKLFDVDSLEKGDARALMNLHNNRAGRLAVRATMRCKCHGISGCSIQTC 194
QY 213 WLQIAEFREMGDYLKAKYDQALKIEMDKROLRAGNSABGHWPDAEFLPSAEALIFLEE 272
DB 195 WLQIAEFREMGDYLKAKYDQALKIEMDKROLRAGNSABGHWPDAEFLPSAEALIFLEE 254
QY 273 SPDYCTCNSSIGIYGTGREGCLONSHNTSRWERRSCGRLCTEGLOVEERKTEVISSCNC 332
DB 255 SPDYCTCNSSIGIYGTGREGCLONSHNTSRWERRSCGRLCTEGLOVEERKTEVISSCNC 314
QY 333 KFWCCTVCKDQCGRHVSKYYCARSPGSAQSLGKGS 369
DB 315 KFWCCTVCKDQCGRHVSKYYCARSPGSAQSLGKGS 351

RESULT 3

US-09-842-758-44
Sequence 44, Application US/09842758
Publication No. US20030083244A1
GENERAL INFORMATION:
APPLICANT: Vernet, Corine A. M.
APPLICANT: Fernandes, Elma R.
APPLICANT: Gerlach, Valerie
APPLICANT: Shimkets, Richard A.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Zernhusen, Bryan D.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Majumder, Kumud
APPLICANT: Tcheneru, Velizar T.
APPLICANT: Padigaru, Muralidhara
APPLICANT: Burgess, Catherine E.
APPLICANT: Gangolli, Esha A.
APPLICANT: Smithson, Glenda
APPLICANT: Rastelli, Luca
APPLICANT: MacDougall, John R.
APPLICANT: Taupier, Raymond J.
APPLICANT: Grose, William M.
APPLICANT: Edward, Szekeres S.
APPLICANT: Alsobrook II, John P.
TITLE OF INVENTION: No. US20030083244A1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-783
CURRENT APPLICATION NUMBER: US/09/842,758
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/200,158
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 60/200,613
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,780
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/201,006
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,007
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,236
PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 60/201,238
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,186
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/201,474
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/201,508
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/220,591
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/232,678
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/263,217
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/265,160
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 44
LENGTH: 355
TYPE: PRT
ORGANISM: Homo sapiens
US-09-842-758-44

Query Match 87.9%; Score 1791; DB 11; Length 355;
Best Local Similarity 97.9%; Pred. No. 5.7e-167;
Matches 327; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 33 CLTSLPGRSVNPLITGPAYLTYTTSVALGAOSGIECKFPFAMERNCPENALQST 92
DB 15 CAAPASAMSVNNFLITGPAYLTYTTSVALGAOSGIECKFPFAMERNCPENALQST 74
QY 93 HNLRSATRETSFIIHAISSAGVWYITKNCMGDPFENCGDGSNNKGTGGHWTGCGSD 152
DB 75 HNLRSATRETSFIIHAISSAGVWYITKNCMGDPFENCGDGSNNKGTGGHWTGCGSD 134
QY 153 NVEFERISKLFPVDSLEKGDARALMNLHNNRAGRLAVRATMKRTCKCHGISGCSIOTC 212
DB 135 NVEFERISKLFPVDSLEKGDARALMNLHNNRAGRLAVRATMKRTCKCHGISGCSIOTC 194
QY 213 WLOAEFREMGDIYKAKYDOLKIEMDKROLRAGNSAGHWPABAFLPSEAEELIFLEE 272
DB 195 WLOAEFREMGDIYKAKYDOLKIEMDKROLRAGNSAGHWPABAFLPSEAEELIFLEE 254
QY 273 SPDYCTCNSSLGIYGTGREGCLONSHNTRMWRSSCGRLCTEGLOYEERKTEVISSCNC 332
DB 255 SPDYCTCNSSLGIYGTGREGCLONSHNTRMWRSSCGRLCTEGLOYEERKTEVISSCNC 314
QY 333 KFWCCTVCKDCQCRHVSKYKCARSPGSAQSLGK 366
DB 315 KFWCCTVCKDCQCRHVSKYKCARSPGSAQSLGK 348

RESULT 4
US-10-285-976-23
Sequence 23, Application US/10285976
Publication No. US20030165500A1
GENERAL INFORMATION:
APPLICANT: Rhee, Chae-Seo
APPLICANT: Malini, Sen
APPLICANT: Wu, Christina
APPLICANT: Leon, Lorenzo M.
APPLICANT: Corr, Maripat
APPLICANT: Carson, Dennis A.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Wnt and Fz12 Receptors as Targets for Immunotherapy
FILE REFERENCE: 023070-130320US
CURRENT APPLICATION NUMBER: US/10/285,976
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US 60/287,995
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: WO PCT/US02/13802

PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 232
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 355
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human Wnt-8a
US-10-285-976-23

Query Match 87.9%; Score 1791; DB 12; Length 355;
Best Local Similarity 97.9%; Pred. No. 5.7e-167;
Matches 327; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 33 CLTSLPGRSVNPLITGPAYLTYTTSVALGAOSGIECKFPFAMERNCPENALQST 92
DB 15 CAAPASAMSVNNFLITGPAYLTYTTSVALGAOSGIECKFPFAMERNCPENALQST 74
QY 93 HNLRSATRETSFIIHAISSAGVWYITKNCMGDPFENCGDGSNNKGTGGHWTGCGSD 152
DB 75 HNLRSATRETSFIIHAISSAGVWYITKNCMGDPFENCGDGSNNKGTGGHWTGCGSD 134
QY 153 NVEFERISKLFPVDSLEKGDARALMNLHNNRAGRLAVRATMKRTCKCHGISGCSIOTC 212
DB 135 NVEFERISKLFPVDSLEKGDARALMNLHNNRAGRLAVRATMKRTCKCHGISGCSIOTC 194
QY 213 WLOAEFREMGDIYKAKYDOLKIEMDKROLRAGNSAGHWPABAFLPSEAEELIFLEE 272
DB 195 WLOAEFREMGDIYKAKYDOLKIEMDKROLRAGNSAGHWPABAFLPSEAEELIFLEE 254
QY 273 SPDYCTCNSSLGIYGTGREGCLONSHNTRMWRSSCGRLCTEGLOYEERKTEVISSCNC 332
DB 255 SPDYCTCNSSLGIYGTGREGCLONSHNTRMWRSSCGRLCTEGLOYEERKTEVISSCNC 314
QY 333 KFWCCTVCKDCQCRHVSKYKCARSPGSAQSLGK 366
DB 315 KFWCCTVCKDCQCRHVSKYKCARSPGSAQSLGK 348

RESULT 5
US-10-005-947-2
Sequence 2, Application US/10005947
Publication No. US20020123103A1
GENERAL INFORMATION:
APPLICANT: Holloway, James L.
TITLE OF INVENTION: Human Wnt Gene
FILE REFERENCE: 99-87
CURRENT APPLICATION NUMBER: US/10/005,947
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: US/09/715,993
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 415
TYPE: PRT
ORGANISM: Homo sapiens
US-10-005-947-2

Query Match 87.5%; Score 1783; DB 14; Length 415;
Best Local Similarity 98.2%; Pred. No. 4.3e-166;
Matches 326; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 33 CLTSLPGRSVNPLITGPAYLTYTTSVALGAOSGIECKFPFAMERNCPENALQST 92
DB 15 CAAPASAMSVNNFLITGPAYLTYTTSVALGAOSGIECKFPFAMERNCPENALQST 74
QY 93 HNLRSATRETSFIIHAISSAGVWYITKNCMGDPFENCGDGSNNKGTGGHWTGCGSD 152
DB 75 HNLRSATRETSFIIHAISSAGVWYITKNCMGDPFENCGDGSNNKGTGGHWTGCGSD 134
QY 153 NVEFERISKLFPVDSLEKGDARALMNLHNNRAGRLAVRATMKRTCKCHGISGCSIOTC 212

Db 135 NVEFERISKLFDVDSLEKGDARALMNLHNNRAGRLAVATMKRTCKCHGISGCSIOTC 194
QY 213 WQLAEFRMGDYLAQKDOALKIEMDKROLRAGNSAEHWPAPAPLPSAEALIFLEE 272
Db 195 WQLAEFRMGDYLAQKDOALKIEMDKROLRAGNSAEHWPAPAPLPSAEALIFLEE 254
QY 273 SPDYCTCNSSLGITGTEGECCLONSHNTSRWERRSCGRLCTEGLQVEERKTEVISSCNC 332
Db 255 SPDYCTCNSSLGITGTEGECCLONSHNTSRWERRSCGRLCTEGLQVEERKTEVISSCNC 314
QY 333 KFOWCCTVCKDCQCRHVSKYTCARSPGSAOSL 364
Db 315 KFOWCCTVCKDCQCRHVSKYTCARSPGSAOSL 346

RESULT 6

US-09-842-758-45
Sequence 45, Application US/09842758
Publication No. US20030083244A1
GENERAL INFORMATION:
APPLICANT: Vernet, Corine A. M.
APPLICANT: Fernandes, Elma R.
APPLICANT: Gerlach, Valerie
APPLICANT: Shinkels, Richard A
APPLICANT: Malyankar, Uriel M
APPLICANT: Boldog, Ferenc L
APPLICANT: Zethusen, Bryan D
APPLICANT: Spytek, Kimberly A
APPLICANT: Majumder, Kumud
APPLICANT: Tchernyev, Vellizar T
APPLICANT: Padigaru, Muralidhara
APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine E
APPLICANT: Gangolli, Esha A
APPLICANT: Smithson, Glennda
APPLICANT: Rastelli, Luca
APPLICANT: MacDougall, John R
APPLICANT: Taupier, Raymond J
APPLICANT: Grose, William M
APPLICANT: Edward, Szekeres S
APPLICANT: Alsbrook II, John P
TITLE OF INVENTION: No. US20030083244A1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-783
CURRENT FILING DATE: 2001-04-25
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/200,158
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 60/200,613
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,780
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/201,006
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,007
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,236
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,238
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,186
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/201,474
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/201,508
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/220,591
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/232,678
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/263,217
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/265,160

PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentl Ver. 2.1
SEQ ID NO 45
LENGTH: 354
TYPE: PRT
ORGANISM: Mus musculus
US-09-842-758-45

Query Match 73.4%; Score 1496; DB 11; Length 354;
Best Local Similarity 82.5%; Pred. No. 4.7e-138;
Matches 269; Conservative 22; Mismatches 35; Indels 0; Gaps 0;

QY 42 SVNNFLITGPXAVLYTTTVALGAOSGIEBCKQFAMERNNCENALQSTHNRLSATR 101
Db 24 SVNNFLITGPXAVLYTTTVALGAOSGIEBCKQFAMERNNCENALQSTHNRLSATR 83
QY 102 ETSFHAIRSAAGWYITTKNCSDGFENCCDGSNNKGTGHWIMGCGSDNVEFERIS 161
Db 84 ETSFHAIRSAAGWYITTKNCSDGFENCCDGSNNKGTGHWIMGCGSDNVEFERIS 143
QY 162 KLFDVDSLEKGDARALMNLHNNRAGRLAVATMKRTCKCHGISGCSIOTCWLQLAERE 221
Db 144 KLFDVDSLEKGDARALMNLHNNRAGRLAVATMKRTCKCHGISGCSIOTCWLQLAERE 203
QY 222 MGDYLAQKDOALKIEMDKROLRAGNSAEHWPAPAPLPSAEALIFLEESPDYCTCNS 281
Db 204 MGDYLAQKDOALKIEMDKROLRAGNSAEHWPAPAPLPSAEALIFLEESPDYCTCNS 263
QY 282 SLGITGTEGECCLONSHNTSRWERRSCGRLCTEGLQVEERKTEVISSCNCQFOWCCTVK 341
Db 264 SLGITGTEGECCLONSHNTSRWERRSCGRLCTEGLQVEERKTEVISSCNCQFOWCCTVK 323
QY 342 CDQCRHVSKYTCARSPGSAOSL 367
Db 324 CDQCRHVSKYTCARSPGSAOSL 349

RESULT 7

US-10-005-947-4
Sequence 4, Application US/10005947
Publication No. US20020123103A1
GENERAL INFORMATION:
APPLICANT: Holloway, James L.
TITLE OF INVENTION: Human Wnt Gene
FILE REFERENCE: 99-87
CURRENT APPLICATION NUMBER: US/10/005,947
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: US/09/715,993
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 354
TYPE: PRT
ORGANISM: Mouse
US-10-005-947-4

Query Match 73.4%; Score 1496; DB 14; Length 354;
Best Local Similarity 82.5%; Pred. No. 4.7e-138;
Matches 269; Conservative 22; Mismatches 35; Indels 0; Gaps 0;

QY 42 SVNNFLITGPXAVLYTTTVALGAOSGIEBCKQFAMERNNCENALQSTHNRLSATR 101
Db 24 SVNNFLITGPXAVLYTTTVALGAOSGIEBCKQFAMERNNCENALQSTHNRLSATR 83
QY 102 ETSFHAIRSAAGWYITTKNCSDGFENCCDGSNNKGTGHWIMGCGSDNVEFERIS 161
Db 84 ETSFHAIRSAAGWYITTKNCSDGFENCCDGSNNKGTGHWIMGCGSDNVEFERIS 143
QY 162 KLFDVDSLEKGDARALMNLHNNRAGRLAVATMKRTCKCHGISGCSIOTCWLQLAERE 221
Db 144 KLFDVDSLEKGDARALMNLHNNRAGRLAVATMKRTCKCHGISGCSIOTCWLQLAERE 203


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Oy      222  MGDTLKKKKYDALKIEMDKROLRAGNSAEGHWVPAEAFPSAEALLFLFEESPQYTCNS 281
Db      204  MGNVLKAKYDPALEKLEIEMDKROLRAGNRAGRWALTEAFLEPTEHELLFLFEESPQYCRNA 263
Oy      282  SLGIYVTEGRECLONSHNTSRWERRSCGRLCTECGLQYVEERKTEVISCNCKFQWCTVK 341
Db      264  SLISIGTEGRECLQNASASASRREORS CGRLCTECGLQYVEERABAVSSCDNFQWCTVK 323
Oy      342  CDQCRHVVSXKYCCARSPESAQSLGK 367
Db      324  CGQCRHVVSRYCTTRPVGSARPRGRG 349

RESULT 8
US-09-842-758-46
Sequence 46, Application US/09842758
Publication No. US20030083244A1
GENERAL INFORMATION:
APPLICANT: Vernet, Corine A. M.
APPLICANT: Fernandez, Elma R.
APPLICANT: Gerlach, Valerie
APPLICANT: Shimkets, Richard A
APPLICANT: Malyankar, Urfel M
APPLICANT: Boldog, Ferenc L
APPLICANT: Zernusen, Bryan D
APPLICANT: Spytek, Kimberly A
APPLICANT: Majumder, Kumud
APPLICANT: Tchiernev, Velizar T
APPLICANT: Padigaru, Muralidhara
APPLICANT: Paturetjan, Meera
APPLICANT: Burgess, Catherine E
APPLICANT: Gangolli, Esna A
APPLICANT: Smithson, Glenda
APPLICANT: Rastelli, Luca
APPLICANT: MacDougall, John R
APPLICANT: Taupier, Raymond J
APPLICANT: Grose, William M
APPLICANT: Edward, Stokeres S
APPLICANT: Alsobrook II, John P
TITLE OF INVENTION: No. US20030083244A1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 1586-783
CURRENT APPLICATION NUMBER: US/09/842,758
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/200,158
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 60/200,613
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,780
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/201,006
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,007
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,236
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,238
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,186
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/201,474
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/201,508
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/220,591
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/232,678
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/263,217
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/265,160
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 113

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-842-758-46

Query Match      68.1%; Score 1388; DB 11; Length 387;
Best Local Similarity 75.3%; Pred.No.2.1e-127;
Matches 244; Conservative 40; Mismatches 40; Indels 0; Gaps 0;

QY CLTFLSLGRSVNNFLITGPKAVYLTYYTSVALGAQSGIEECKFPQFAMERNWPCENALQLST 92
Db      16 CPEPTASAMVNNFLMTGPKAVYLTYSASVAVGANGIEECKYQFAMERNWCPSTLQLAT 75
QY      93 HNRLSRSTRSTSTTHAISAAGVMIITKNCWGDGFENCGCDSSNGKTGSHGMIWGCGSD 152
Db      76 HNGRSRSTRSTSTFVHAISAAGVMIITLRNCWMDPFNCCDDSDRNGRIIGRGVWVGCGSD 135
QY      153 NVEEGERISLTPDLSIEKGDARALNNLHNRAGRLAVRATMKTCTCKCHGISGSCSIQTC 212
Db      136 NAEGERISLTPDGLLETQDARALNNLHNRAGRLAVKETMRTCTCKCHGISGSCSIQTC 195
QY      213 WLQALREKMGDYLKAKYDQALKTENDKROLRAGNSAEHGWVPAEAFPLPSAEALLFLFE 272
Db      196 WLQALREKMGDYLKAKYDQALKTENDKROLRAGNSAEHGWVPAEAFPLPSAEALLFLFE 255
QY      273 SPDYCTCNSSLGIVTEGREGCLQNSHNTSRWERRSCGRCTCEGLOVEKTEVISSCNC 332
Db      256 SPDYCLKNISLIGVTEGREGCLQSGKNLSQWERRSCGRCTCEGLOVEKTEVISSCNC 315
QY      333 KFMQCTVKKCDQCRHVYSKYYCAR 356
Db      316 KFMQCTVKKCDQCRHVYSKYYCAR 339

RESULT 9
US-09-842-758-47
; Sequence 47, Application US/09842758
; Publication No. US20030083244A1
; GENERAL INFORMATION:
; APPLICANT: Verner, Corine A. M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shinkets, Richard A
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zorhausen, Bryan D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Padigarau, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E
; APPLICANT: Gangoili, Beha A
; APPLICANT: Smithson, Glenda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R
; APPLICANT: Taupier, Raymond J
; APPLICANT: Grose, William M
; APPLICANT: Edward, Szekeres S
; APPLICANT: Alsobrook II, John P
; TITLE OF INVENTION: No. US20030083244A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-783
; CURRENT APPLICATION NUMBER: US/09/842,758
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/200,158
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,613
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,780
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/201,006

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PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,007
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,236
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,238
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,186
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/201,474
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/201,508
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/220,591
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/232,678
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/263,217
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/265,160
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 357
TYPE: PRT
ORGANISM: Gallus gallus
US-09-842-758-47

Query Match 67.7%; Score 1379; DB 11; Length 357;
Best Local Similarity 76.5%; Pred. No. 1.4e-126;
Matches 241; Conservative 37; Mismatches 37; Indels 0; Gaps 0;

42 SVNNFLITGPKAYLYTTTSVALGAOSGIEBCKFOFAMERNKCPNALOLSTHNRLSRSTR 101
25 SVNNFLMTGPKAYLYTSSVAAGAOSGIEBCKFOFAMERNKCPNALOLSTHNRLSRSTR 84
102 ETSFIHAISSAGVWYITRKNCMDGFENCGCGDSNNGKTGHWIMGCSDNVEFGERIS 161
85 ETSFVHAISSAGVWYITLRNCSLDGFESCGCDSRNGRGVWGCSDNVEFGERIS 144
162 KLPVDSLEKGDAPALNMLNHNRAQLAVRATMRKTCGHSIGSCSIQTCLWLAERRE 221
145 KLPVDALETGHDFTALIMLNHNNEVGRILAVKATMKRACKCHGVSGCSIQTCWLADPRE 204
222 MGDIKAKYDQALXIEMDKROLRAAGNSAEGHWVPAEALFLPABELFLESPPDYCTNS 281
205 IGVLYKMYDQAHKLEMDKRRMRAGNSADSRGATRETFHVHSTELVLEDSPPDYCTRNA 264
282 SLGIYTEGRECLONSHNTSWERRSCRLCTECGLQVEERKTEVSISSCNCKFOMCCTVK 341
265 SLGHGTEGRECLQTKGKLSQWERRSCRLTEGCLKVEERTEVSSCNCKFHMCCIVR 324
342 CDQCRHVSVSKYYCAR 356
325 CECROLVAKHFCAR 339

RESULT 10
US-10-285-976-25
Sequence 25, Application US/10285976
Publication No. US20030165500A1
GENERAL INFORMATION:
APPLICANT: Rhee, Chae-Seo
APPLICANT: Malini, Sen
APPLICANT: Wu, Christina
APPLICANT: Leonil, Lorenzo M.
APPLICANT: Corr, Maripat
APPLICANT: Carson, Dennis A.
TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
TITLE OF INVENTION: In Head and Neck Squamous Cell Carcinomas
FILE REFERENCE: 023070-130320US

CURRENT APPLICATION NUMBER: US/10/285,976
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US 60/287,995
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: WO PCT/US02/13802
PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 232
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LENGTH: 351
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human wnt-8b
US-10-285-976-25

Query Match 59.5%; Score 1213; DB 12; Length 351;
Best Local Similarity 63.8%; Pred. No. 2.6e-110;
Matches 220; Conservative 44; Mismatches 71; Indels 10; Gaps 3;

26 CLPIHLCITFSLFGSSVNNFLITGPKAYLYTTTSVALGAOSGIEBCKFOFAMERNKCP 85
11 CLPIHLCITFSLFGSSVNNFLITGPKAYLYTSSVAAGAOSGIEBCKFOFAMERNKCP 67
86 NALQSTHNRLSRSTRSTFIHAISSAGVWYITRKNCMDGFENCGCGDSNNGKTGHW 145
68 NALQSTHNRLSRSTRSTFIHAISSAGVWYITLRNCSLDGFENCGCGDSRNGRGVWGC 127
146 IGGCSNVEFGERISLTFPDSLEKGDAPALNMLNHNRAQLAVRATMRKTCGHSIG 205
128 IGGCSNVEFGERISLTFPDSLEKGDAPALNMLNHNRAQLAVRATMRKTCGHSIG 187
206 SCSTQTCWLQAEFFREMGDIKAKYDQALXIEMDKROLRAAGNSAEGHWVPAEALFLP 265
188 SCSTQTCWLQAEFFREMGDIKAKYDQALXIEMDKROLRAAGNSAEGHWVPAEALFLP 244
266 ELIFLESPPDYCTNSSLGIYTEGRECLONSHNTSWERRSCRLCTECGLQVEERKTE 325
245 ELVHLEDSPPDYCTNSSLGIYTEGRECLONSHNTSWERRSCRLCTECGLQVEERKTE 304
326 VISSCNCKFOMCCTVKCDQCRHVSVSKYYCARSP-----GSNOSLGK 366
305 TVSSCNCKFOMCCTVKCDQCRHVSVSKYYCARSP-----GSNOSLGK 349

RESULT 11
US-10-005-947-6
Sequence 6, Application US/10005947
Publication No. US20020123103A1
GENERAL INFORMATION:
APPLICANT: Holloway, James L.
TITLE OF INVENTION: Human Wnt Gene
FILE REFERENCE: 99-87
CURRENT APPLICATION NUMBER: US/10/005,947
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: US/09/715,993
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 295
TYPE: PRT
ORGANISM: Homo sapiens
US-10-005-947-6

Query Match 55.8%; Score 1137.5; DB 14; Length 295;
Best Local Similarity 68.0%; Pred. No. 5.2e-103;
Matches 202; Conservative 35; Mismatches 57; Indels 3; Gaps 1;

42 SVNNFLITGPKAYLYTTTSVALGAOSGIEBCKFOFAMERNKCPNALOLSTHNRLSRSTR 101
25 SVNNFLMTGPKAYLYTSSVAAGAOSGIEBCKFOFAMERNKCPNALOLSTHNRLSRSTR 84


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RESULT 14
US-10-285-976-15
; Sequence 15, Application US/10285976
; Publication No. US20030165500A1
; GENERAL INFORMATION:
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Malini, Sen
; APPLICANT: Wu, Christina
; APPLICANT: Leonil, Lorenzo M.
; APPLICANT: Corr, Maripat
; APPLICANT: Carson, Dennis A.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Wnt and Frizzled Receptors as targets for Immunotherapy
; FILE REFERENCE: 023070-130320US
; CURRENT APPLICATION NUMBER: US/10/285,976
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/287,995
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: WO PCT/US02/13802
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human wnt-5b
US-10-285-976-15

Query Match      31.9%; Score 649.5; DB 12; Length 359;
Best Local Similarity 40.8%; Pred. No. 4.6e-55;
Matches 127; Conservative 49; Mismatches 108; Indels 27; Gaps 7;

QY 54 YLTGTTVALGAGSGIECKGFOPAMERNCPENALQSTHNR-LRSATRETSFIHAISAA 112
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 YQEHMAYIGBAKGTGKECOHQFORRMWC-STADNASVFGRWVQIGSRRTAFTHAVSAA 123

QY 113 GWMYITFNKSGMDPFCNGCGDSNNGKTGCGHGWIMGCGSDNVEGERISKLFDVDSLEKX 172
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 GVNVAISRACREBELSTGCGSRTARPKDLPRDMLMGCGGDNVEGYFAKEFVDAREK 183

QY 173 D-----APALMNLHNNRAGRLAVRATMKRTCKCHGISGCSIQTCWLQLAFFREMGD 224
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 184 NFAKSEEGRGVLMNLQNNBAGRRAVYKMDVACKCHGVSGCSILKTCWLQLAFFRYGD 243

QY 225 YLKAKYDQALKIENDKR-QLRAGNSAEGHWVPAEAFPLSAEALIFLEESPDYCTCNSSL 283
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 RLKEKYDAAAMRVTRKGRLELVNS-----RFTQPTPEDLVVYDPPDYCLRNES 294

QY 284 GIVTEGREGCLONSHNTRMWRSSCGRLCTECGLQVERKTEVVISCNCKFQWOCCTVYKCD 343
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 295 GSLGTQGRLCNKTSSEGD-----GCELMC--CGRGYNQFASVVERCHCKFHWCCFVRCK 347

QY 344 QCRHVVSXKYC 354
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 348 KCTEIVDQYIC 358

RESULT 15
US-10-295-027-584
; Sequence 584, Application US/10295027
; Publication No. US2003023250A1
; GENERAL INFORMATION:
; APPLICANT: Afari, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezil, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard

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; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 584
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-584

Query Match      31.9%; Score 649.5; DB 12; Length 359;
Best Local Similarity 40.8%; Pred. No. 4.6e-55;
Matches 127; Conservative 49; Mismatches 108; Indels 27; Gaps 7;

QY 54 YLTGTTVALGAGSGIECKGFOPAMERNCPENALQSTHNR-LRSATRETSFIHAISAA 112
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 YQEHMAYIGBAKGTGKECOHQFORRMWC-STADNASVFGRWVQIGSRRTAFTHAVSAA 123

QY 113 GWMYITFNKSGMDPFCNGCGDSNNGKTGCGHGWIMGCGSDNVEGERISKLFDVDSLEKX 172
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 GVNVAISRACREBELSTGCGSRTARPKDLPRDMLMGCGGDNVEGYFAKEFVDAREK 183

QY 173 D-----APALMNLHNNRAGRLAVRATMKRTCKCHGISGCSIQTCWLQLAFFREMGD 224
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 184 NFAKSEEGRGVLMNLQNNBAGRRAVYKMDVACKCHGVSGCSILKTCWLQLAFFRYGD 243

QY 225 YLKAKYDQALKIENDKR-QLRAGNSAEGHWVPAEAFPLSAEALIFLEESPDYCTCNSSL 283
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 RLKEKYDAAAMRVTRKGRLELVNS-----RFTQPTPEDLVVYDPPDYCLRNES 294

QY 284 GIVTEGREGCLONSHNTRMWRSSCGRLCTECGLQVERKTEVVISCNCKFQWOCCTVYKCD 343
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 295 GSLGTQGRLCNKTSSEGD-----GCELMC--CGRGYNQFASVVERCHCKFHWCCFVRCK 347

QY 344 QCRHVVSXKYC 354
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 348 KCTEIVDQYIC 358

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Search completed: January 30, 2004, 13:35:48
 Job time : 41 secs

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OM protein - protein search, using SW model

Run on: January 30, 2004, 13:29:15 ; Search time 23 Seconds
(without alignments)
1215.200 Million cell updates/sec

Title: US-09-898-456-7
Perfect score: 2037
Sequence: 1 MLCICICLVSPFPTLTPC.....SKYYCARSPGASQSLKGSA 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 367270 seqs, 75744148 residues

Total number of hits satisfying chosen parameters: 367270

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_US03-37355-58
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1808	88.8	351	1	PCT-US03-37355-58
2	1804	88.6	351	6	US-10-451-168-62
3	1791	87.9	355	1	PCT-US03-31384-21
4	1791	87.9	355	1	PCT-US03-31384-21
5	1213	59.5	351	1	PCT-US03-31384-22
6	1213	59.5	351	1	PCT-US03-31384-22
7	650.5	31.9	351	1	PCT-US03-31384-27
8	650.5	31.9	351	1	PCT-US03-31384-27
9	649.5	31.9	359	1	PCT-US03-31384-17
10	649.5	31.9	359	1	PCT-US03-31384-17
11	649.5	31.9	359	5	US-09-976-858-88
12	648	31.8	351	1	PCT-US03-31384-15
13	648	31.8	351	7	US-60-485-101-623
14	648	31.8	351	7	US-60-485-101-623
15	644	31.6	351	7	US-60-485-101-691
16	644	31.6	351	7	US-60-485-101-691
17	640.5	31.4	360	1	PCT-US03-31384-8
18	640.5	31.4	360	1	PCT-US03-31384-8
19	640.5	31.4	360	1	PCT-US03-31384-8
20	636.5	31.2	338	1	US-10-454-246-178
21	636.5	31.2	338	6	US-10-454-246-178
22	636.5	31.2	365	1	PCT-US03-37355-56
23	636.5	31.2	365	1	PCT-US03-17512-176
24	636.5	31.2	365	1	PCT-US03-31384-16
25	636.5	31.2	365	1	PCT-US03-31384-16
26	636.5	31.2	365	6	US-10-474-291-13

27	636.5	31.2	365	6	US-10-454-246-176	Sequence 176, App
28	636	31.2	370	1	PCT-US03-37355-50	Sequence 50, App1
29	636	31.2	370	1	PCT-US03-31384-1	Sequence 1, App1
30	636	31.2	370	1	PCT-US03-31384-1	Sequence 1, App1
31	636	31.2	370	7	US-60-505-218-524	Sequence 524, App
32	626	30.7	334	1	PCT-US03-25100-148	Sequence 148, App
33	626	30.7	352	1	PCT-US03-25100-192	Sequence 192, App
34	626	30.7	355	1	PCT-US03-37355-54	Sequence 54, App1
35	626	30.7	355	1	PCT-US03-31384-13	Sequence 13, App1
36	626	30.7	355	1	PCT-US03-31384-13	Sequence 13, App1
37	625	30.7	334	1	PCT-US03-25100-160	Sequence 160, App
38	625	30.7	338	1	PCT-US03-25100-142	Sequence 142, App
39	625	30.7	352	1	PCT-US03-31384-14	Sequence 14, App1
40	625	30.7	352	1	PCT-US03-31384-14	Sequence 14, App1
41	625	30.7	352	1	PCT-US03-25100-140	Sequence 140, App
42	625	30.7	352	1	PCT-US03-25100-144	Sequence 144, App
43	625	30.7	352	1	PCT-US03-25100-146	Sequence 146, App
44	625	30.7	352	1	PCT-US03-25100-152	Sequence 152, App
45	625	30.7	352	1	PCT-US03-25100-156	Sequence 156, App

ALIGNMENTS

RESULT 1
PCT-US03-37355-58
Sequence 58, Application PC/TUS0337355
GENERAL INFORMATION:
APPLICANT: Keating et al.
TITLE OR INVENTION: COMPOSITIONS AND METHODS FOR CELL DIFFERENTIATION AND TISSUE
FILE REFERENCE: HYDR-PWI-004
CURRENT APPLICATION NUMBER: PCT/US03/37355
CURRENT FILING DATE: 2003-11-21
NUMBER OF SEQ. ID NOS: 78
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58
LENGTH: 351
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US03-37355-58

Query Match 88.8%; Score 1808; DB 1; Length 351;
Best Local Similarity 98.2%; Pred. No. 1e-137;
Matches 331; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	33	CLTFLSFGSNNFLITGPAYLTYYTSVALGASGIECKFPQFAMRNCPENALQST	92
DB	15	CAAFSASAMVNNPLITGPAYLTYYTSVALGASGIECKFPQFAMRNCPENALQST	74
QY	93	HNRLRSATRETSPIHAISAGVNYITKNCMDGFENCGDGSNNGTGHWIMGCS	152
DB	75	HNRLRSATRETSPIHAISAGVNYITKNCMDGFENCGDGSNNGTGHWIMGCS	134
QY	153	NVEFGERISLTFVDSLEKGDARALNNHNRAGRLAVRAITMRTCKCHGISGCS	212
DB	135	NVEFGERISLTFVDSLEKGDARALNNHNRAGRLAVRAITMRTCKCHGISGCS	194
QY	213	WLOLAERRENDVLKAKYDOLAKIEMDKROLRAGNSBEGHWVPAEALPBAEMLTLE	272
DB	195	WLOLAERRENDVLKAKYDOLAKIEMDKROLRAGNSBEGHWVPAEALPBAEMLTLE	254
QY	273	SPDYCTNSSLIGYTGREGCLONSHNTSRMERRSCGRLCTEGCLQVEERKTEV	332
DB	255	SPDYCTNSSLIGYTGREGCLONSHNTSRMERRSCGRLCTEGCLQVEERKTEV	314
QY	333	KFQWCTVCKDCQGRHVSKYYCARSPGASQSLKGSA	369
DB	315	KFQWCTVCKDCQGRHVSKYYCARSPGASQSLKGSA	351

RESULT 2
US-10-451-168-62

; Sequence 62, Application US/10451168
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: G50039
; CURRENT APPLICATION NUMBER: US/10/451,168
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US01/49232
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,710
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/257,048
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/260,482
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/264,922
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/266,797
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/276,988
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/281,535
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/289,622
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-451-168-62

Query Match 88.6%; Score 1804; DB 6; Length 351;
Best Local Similarity 97.9%; Pred. No. 2,1e-137;
Matches 330; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 33 CLTFSLGRSVNNFLITGPKAYLTYTTSVALGAOSGIECKFPFAMERWNCPEVALQST 92
DB 15 CAAPSASAMSVNNFLITGPKAYLTYTTSVALGAOSGIECKFPFAMERWNCPEVALQST 74
QY 93 HNRLRSATRETSFTHAISSAGVMYIITKNCMDGFENCGDGSNNKGTGHWIWGCS 152
DB 75 HNRLRSATRETSFTHAISSAGVMYIITKNCMDGFENCGDGSNNKGTGHWIWGCS 134
QY 153 NVEFGERISKLPVDSLEKGDARALMNLHNNRAGRLAVRATMKRTCKCHGISGCSIQTC 212
DB 135 NVEFGERISKLPVDSLEKGDARALMNLHNNRAGRLAVRATMKRTCKCHGISGCSIQTC 194
QY 213 WLQIAEFREMGDYKAKYDQALKIEMDRQLRAGNSAGHWVPAEAPLPSAEALIFLEE 272
DB 195 WLQIAEFREMGDYKAKYDQALKIEMDRQLRAGNSAGHWVPAEAPLPSAEALIFLEE 254
QY 273 SPDYCTCNSSLGIGYTGREGCLONSHNTSRWERSRCGLCTEGCLQYERKTEVISSCNC 332
DB 255 SPDYCTCNSSLGIGYTGREGCLONSHNTSRWERSRCGLCTEGCLQYERKTEVISSCNC 314
QY 333 KFWMCCTVCKDQCRHVVSXYKCARSPGSAQSLGKSA 369
DB 315 KFWMCCTVCKDQCRHVVSXYKCARSPGSAQSLGKSA 351

RESULT 3
PCT-US03-31384-21
; Sequence 21, Application PC/TUS0331384
; GENERAL INFORMATION:
; APPLICANT: He, Biao
; APPLICANT: You, Liang
; APPLICANT: Xu, Zhidong
; APPLICANT: Jablons, David M.
; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Methods for Treating Cancer by Inhibiting Wnt Signaling
; FILE REFERENCE: 023070-125630PC
; CURRENT APPLICATION NUMBER: PCT/US03/31384
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 10/264,825
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US 60/491,350
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human wingless-type 8A (wnt-8A) peptide sequence
PCT-US03-31384-21

Query Match 87.9%; Score 1791; DB 1; Length 355;
Best Local Similarity 97.9%; Pred. No. 2,4e-136;
Matches 327; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 33 CLTFSLGRSVNNFLITGPKAYLTYTTSVALGAOSGIECKFPFAMERWNCPEVALQST 92
DB 15 CAAPSASAMSVNNFLITGPKAYLTYTTSVALGAOSGIECKFPFAMERWNCPEVALQST 74
QY 93 HNRLRSATRETSFTHAISSAGVMYIITKNCMDGFENCGDGSNNKGTGHWIWGCS 152
DB 75 HNRLRSATRETSFTHAISSAGVMYIITKNCMDGFENCGDGSNNKGTGHWIWGCS 134
QY 153 NVEFGERISKLPVDSLEKGDARALMNLHNNRAGRLAVRATMKRTCKCHGISGCSIQTC 212
DB 135 NVEFGERISKLPVDSLEKGDARALMNLHNNRAGRLAVRATMKRTCKCHGISGCSIQTC 194
QY 213 WLQIAEFREMGDYKAKYDQALKIEMDRQLRAGNSAGHWVPAEAPLPSAEALIFLEE 272
DB 195 WLQIAEFREMGDYKAKYDQALKIEMDRQLRAGNSAGHWVPAEAPLPSAEALIFLEE 254
QY 273 SPDYCTCNSSLGIGYTGREGCLONSHNTSRWERSRCGLCTEGCLQYERKTEVISSCNC 332
DB 255 SPDYCTCNSSLGIGYTGREGCLONSHNTSRWERSRCGLCTEGCLQYERKTEVISSCNC 314
QY 333 KFWMCCTVCKDQCRHVVSXYKCARSPGSAQSLGK 366
DB 315 KFWMCCTVCKDQCRHVVSXYKCARSPGSAQSLGK 348

RESULT 4
PCT-US03-31384-21
; Sequence 21, Application PC/TUS0331384
; GENERAL INFORMATION:
; APPLICANT: He, Biao
; APPLICANT: You, Liang
; APPLICANT: Xu, Zhidong
; APPLICANT: Jablons, David M.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Methods for Treating Cancer by Inhibiting Wnt Signaling
; FILE REFERENCE: 023070-125630PC
; CURRENT APPLICATION NUMBER: PCT/US03/31384
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: US 10/264,825
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US 60/491,350
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human wingless-type 8A (wnt-8A) peptide sequence
PCT-US03-31384-21